

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: July 21, 2002, 14:58:48 ; Search time 12014.9 Seconds

(without alignments)
17965.795 Million cell updates/sec

Title: US-09-702-216-1

Perfect score: 10315
Sequence: 1 ttctctcggaaggtctctt.....gttatctcaaaaaaaaaa 10315

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	8				

1	10011	97.1	10011	9	AF183810	AF183810 Homo sapi
2	6756.2	65.5	165813	2	AC013815	AC013815 Homo sapi
3	6595.6	63.9	159505	2	AC023142	AC023142 Homo sapi
4	5295	51.3	5507	9	AF264794	AF264794 Homo sapi
5	3491.2	33.8	4452	10	AF346836	AF346836 Mus muscu
6	2486.4	24.1	2596	5	AK000948	AK000948 Homo sapi
7	2295	22.2	4625	5	AF346838	AF346838 Xenopus l
8	1580.6	15.3	1587	9	AK021511	AK021511 Homo sapi
9	1537	14.9	1551	9	AK021470	AK021470 Homo sapi
10	1423	13.8	165191	5	AF346837	AF346837 Xenopus l
11	1306	12.7	3767	2	AC03571	AC03571 Homo sapi
12	1139.4	11.0	82724	2	AC084171	AC084171 Homo sapi
13	1139.4	11.0	310002	2	AF178030	AF178030 Homo sapi
14	1116	10.8	165191	2	AC103571	AC103571 Rattus no
15	943.4	9.1	996	6	AX067304	AX067304 Sequence
16	771.2	7.5	113725	2	AC108615	AC108615 Rattus no
17	761.4	7.4	766	6	AX113088	AX113088 Rattus no
18	668.8	6.5	674	6	AX067327	AX067327 Sequence
19	460.8	4.5	350004	9	AF130342	AF130342 Homo sapi
20	457.6	4.4	113725	2	AC108615	AC108615 Rattus no
21	275.4	2.7	305	6	AX156253	AX156253 Sequence
22	258.4	2.5	67407	2	AC013789	AC013789 Homo sapi
23	94	0.9	82724	2	AC084171	AC084171 Homo sapi
24	93.4	0.9	67407	2	AC013789	AC013789 Homo sapi
25	89.4	0.9	22448	2	PFMAL4P4	PFMAL4P4 Plasmodiu
26	81.8	0.8	53932	2	AC023371	AC023371 Homo sapi
27	79.4	0.8	7355	6	AX344889	AX344889 Sequence
28	79.4	0.8	130540	6	AC079417	AC079417 Mus muscu
29	79.2	0.8	349980	6	AX344563	AX344563 Sequence
30	78.8	0.8	321003	2	PFMAL4P3	PFMAL4P3 Plasmodiu
31	78.4	0.8	8079	6	AX356488	AX356488 Sequence
32	77.8	0.8	4865	3	AF364131	AF364131 Anopheles
33	77.8	0.8	12405	6	AX21840	AX21840 Sequence
34	77.8	0.8	12405	6	AX277872	AX277872 Sequence
35	77.8	0.8	12405	6	AX323555	AX323555 Sequence
36	77.8	0.8	22243	3	PFVARK23A	PFVARK23A Plasmodiu
37	77.4	0.8	5126	6	AX348926	AX348926 Sequence
38	77.4	0.8	83440	2	AC024285	AC024285 Homo sapi
39	77	0.7	192929	2	AC005505	AC005505 Plasmodiu
40	77	0.7	256172	2	AC005139	AC005139 Plasmodiu
41	77	0.7	310779	2	AC005140	AC005140 Plasmodiu
42	76.8	0.7	349980	6	AX344566	AX344566 Sequence
43	76.6	0.7	1141	6	AX083744	AX083744 Sequence
44	76.4	0.7	184535	2	CNS05TCU	AL351100 Homo sapi
45	76.2	0.7	99003	2	AL390756	AL390756 Homo sapi

ALIGNMENTS

RESULT 1
AF183810
LOCUS AF183810 10011 bp mRNA linear PRI 10-JAN-2000
DEFINITION Homo sapiens zinc finger transcription factor TRF1 mRNA, complete cds.
ACCESSION AF183810
VERSION AF183810.1 GI:6684533
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 10011)
Momeni, P., Gloeckner, G., Schmidt, O., von Holtum, D., Albrecht, B.,
Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,
Rosenthal, A., Horsthemke, B. and Ludecke, H.-J.
Mutations in a new gene, encoding a zinc-finger protein, cause
tricho-rhino-phalangeal syndrome type I

TITLE

JOURNAL Nat. Genet. 24 (1), 71-74 (2000)

MEDLINE 2 (bases 1 to 10011)

REFERENCE

AUTHORS Momeni, P., Gloeckner, G., Schmidt, O., von Holtum, D., Albrecht, B.,
Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,
Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,

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DB 1501 ctgcgtgtccgcacagacatcaattctcaagccgttttactaatgagaccatgag 1560
QY 1561 lgaagtgacttccagtgagaaacatcattggcattgagcggaaacacagattggcaag 1620
DB 1561 tgcagtgacttccagtgagaaacatcattggcattgagcggaaacacagattggcaag 1620
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DB 1621 ggaacacagatttccgcgtgtaatttactatgaggggaactatcca 1680
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DB 1801 ccagtgacttctgagacttgggaaatggcagacagatataacagtcagaagagatg 1860
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DB 1861 acaactcctglttggactcaagtgccataaagccctcgtatctctctagacaaatgta 1920
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DB 1921 cagaagccacacagtlactactggtgtaatttctgacttccagctgtagactagct 1980
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DB 1981 caacttaactgtagaacaacttctgagcagcagcagcagcagcagcagcagcagcagc 2040
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DB 2221 gtagcttccatattccaaaagccatggccctgattgaatgtagtggggccactctcc 2280
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Qy 5821 ttaataatllcatatattgllcccaacagtagttatlltlltgcacagagatgtag 5880
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Db 5821 TTTAATTAATTTGCAATTAATTAATTTGTCACACAGACTAGTATTTTGGCCAGAGATGTAG 5880

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Db	5881	AAGATATTACAAGCTACGGAGATCGACTGTCAGATTAACTTATTTCAATTAAGCAAGCTTGGG	5940
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ORGANISM	Homo sapiens		
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AUTHORS	Britten R. (1985)		

TITLE Homo sapiens chromosome 8, clone RP11-21J16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165813)
AUTHORS

Britten, R., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Bana, N., Beckert, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardina, S., Grant, G., Haggis, B., Heath, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kahn, L., Karas, A., Klein, J., Lehoczy, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDonald, J., Melnick, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange, R., Stojanovic, N., Stromman, A., Talamas, J., Testa, Y., Tittell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jan 20, 2002 this sequence version replaced gi:16931009. All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WMR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: LA033

Center clone name: 21_J16

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 19659: contig of 19659 bp in length
* 19660 19759: gap of 100 bp
* 19760 114181: contig of 94422 bp in length
* 114182 114281: gap of 100 bp
* 114282 143282: contig of 29001 bp in length
* 143283 143382: gap of 100 bp
* 143383 165813: contig of 22431 bp in length.

FEATURES

Location/Qualifiers

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/chromosome="8"
/map="8"

/clone="RP11-21J16"

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ORIGIN

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Best local similarity 99.1%; Pred. No. 0;
Matches 6873; Conservative 0; Mismatches 15; Indels 49; Gaps 6;

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DB 3482 aacaagaagcgccttaacccagagccttcagcgtcagcagctcaacaacagcagc 3541
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DEFINITION Homo sapiens chromosome 8 clone RP11-558B2, WORKING DRAFT SEQUENCE.
ACCESSION  AC023142
VERSION     AC023142.4  GI:9795980
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 159505)
            Waterston,R.H.
            The sequence of Homo sapiens clone
            Unpublished
            2 (bases 1 to 159505)
            Waterston,R.H.
            Direct Submission
            Submitted (08-FEB-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Aug 11, 2000 this sequence version replaced gi:9558667.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H_NH0558B02
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-Primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152349 bases at least Q40
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Consensus quality: 141000; agarose-fp
Insert size: 157705; sum-of-ctnigs
Quality coverage: 4.80 in Q20 bases; agarose-fp
Quality coverage: 4.85 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1432: contig of 1432 bp in length
* 1433 1532: gap of unknown length

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FEATURES

SOURCE

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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 0;
Matches 6666; Conservative 0; Mismatches 14; Indels 12; Gaps 5;

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ACCESSION AF264784
VERSION AF264784.1 GI:10644121
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
AUTHORS Chang,G.T.G., Steenbeck,M., Schippers,F., Blok,L.J., van
Weerden,W.M., van Alewijk,D.C., Bussen,B.H., van Steenbrugge,G.J.
and Brinkmann,A.O.
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Apoptosis in Prostate Cancer Cells
J. Natl. Cancer Inst. 92 (17), 1414-1421 (2000)
10974077
JOURNAL 2 (bases 1 to 5507)
PUBMED 2 (bases 1 to 5507)
AUTHORS Chang,G.T.G.
JOURNAL Direct Submission
Submitted (09-MAY-2000) Endocrinology & Reproduction, Erasmus
University Rotterdam, P.O.Box 1738, Rotterdam 3000 DR, Netherlands
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BASE COUNT 1694 a 1213 c 1234 g 1366 t
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Query Match 51.3%, Score 5295; DB 9; Length 5507;
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RESUME

5

LOCUS

AF346836

DEFINITION

AF346836

ACCESSION

AF346836

VERSION

AF346836.1

KEYWORDS

AF346836.1

SOURCE

GI:13785800

ORGANISM

house mouse.

REFERENCE

Mus musculus

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

1 (bases 1 to 4452)

JOURNAL

EMBO J. 20 (7), 1715-1725 (2001)

PUBMED

11285235

AUTHORS

2 (bases 1 to 4452)

TITLE

Direct Substitution

JOURNAL

Submitted (08-FEB-2001)

FEATURES

Adult Oncology, Dana Farber Cancer Institute, 44 Binney Street, SM 854, Boston, MA 02115, USA

source

Location/Qualifiers

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AK000948

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 REFERENCE 1 (sites)
 AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
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 NBD human cDNA sequencing project
 TITLE Unpublished (2000)
 JOURNAL 2 (bases 1 to 2596)
 REFERENCE Isogai, T. and Otsuki, T.
 TITLE Direct Submission
 AUTHORS Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
 NBD human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan: cDNA full insert
 construction, 5'- & 3'-end one pass sequencing and clone selection:
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.
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REFERENCE			
AUTHORS	Malik,T.H., Sholcnet,S.A., Latham,P., Kroll,T.G., Peters,L.L. and Shivasani,R.A.		
TITLE	Transcriptional repression and developmental functions of the atypical vertebrate GATA protein trps1		
JOURNAL	EMBO J. 20 (7), 1715-1725 (2001)		
PUBMED	11285235		
REFERENCE			
AUTHORS	2 (bases 1 to 4625)		
TITLE	Malik,T.H. and Shivasani,R.A.		
JOURNAL	Submitted (08-FEB-2001) Adult Oncology, Dana Farber Cancer Institute, 44 Binney Street, SM 854, Boston, MA 02115, USA		
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RESULT 8
AK021511
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DEFINITION Homo sapiens cDNA FLJ11449 fis, clone HEMBA1001411.
ACCESSION AK021511
VERSION AK021511.1 GI:10432707
KEYWORDS oligo capping; fts (full insert sequence).
SOURCE Homo sapiens embryonic, 10 weeks whole embryo, mainly head cDNA to
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (sites)

Nishikawa, T., Ueda, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, I., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Maestusa, M., Hatanashi, K., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Omo, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagaike, K., Masuno, Y., Nimomiya, K. and Iwayanagi, T. NEON human cDNA sequencing project

NEO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 1587)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao

NEDO human DNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing, 5'- and 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

location/Qualifiers

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QY 8068 ttatgtgaagtagatcttttataaacaagcatgggattctttcttaagtaataattaat 8127

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RUNOUT 9
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DEFINITION AK021470
ACCESSION AK021470
KEYWORDS Oligo capping; fis (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone lib:HEMBA1 clone:HEMBA1000822.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Magatsuna,M., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takehashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Matenabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,T., Saito,K., Yamamoto,Y., Wakamatsu,A.,
Nakamura,Y., Nagahara,K., Masuhara,Y., Ninomiya,K. and Iwayanagi,T.
NEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 1551)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao
Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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 DEFINITION Homo sapiens chromosome 8 clone CTD-2183P16 map 8, WORKING DRAFT
 SEQUENCE, 2 ordered pieces.
 ACCESSION AC084171
 VERSION AC084171.2 GI:12963014
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 82724)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 8, clone CTD-2183P16
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 82724)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bedalov, F., Boguski, M.,
 Boukhalter, B., Brown, A., Burkett, G., Campiano, A., Castle, A.,

11.08; Score 1139.4; DB 2; Length 82724;

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ACIO3571/c	LOCUS	DEFINITION	VERSION	KEYWORDS	
ACIO3571.2	GI:17975672	Rattus norvegicus clone CH230-22014, *** SEQUENCING IN PROGRESS	ACIO3571	HMG; HMG-PHASEL.	
SOURCE	ORGANISM				
Norway rat. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
Rattus.					
REFERENCE	AUTHORS				
1 (bases 1 to 165191)	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alspbrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbafala,J., Benton,J., Blumage,K., Blankenburg,K., Bonini,D., Bouck,J., Bowler,S., Briena,M., Brown,E., Brown,M., Bryant,N.P., Bubay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.E., Carter,W., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox/C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.I., Davis,C., Day-Carroll,L., Deredich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Din,h.H., Douthwaite,K.J., Draper,H., Dugan-Hochs,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.B., Guetara,M., Gudaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollaway/C., Hollins,B., Homsj,F., Howard,S., Huber,J., Hulky,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivett,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryak,J., Kovar,C., Kratochv,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Louised,H., Lozado,R.J., Lu,X., Lucier,A., Lucifer,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M., Miner,G., Minner,Z., Mitchell,T., Mohabbat,K., Morjan,M., Morris,S., Koser,K., Neal,D., Newton,S., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenkwo,S., Ogun,M., Okunoyen,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L., Qullis,M., Ren,Y., Rives,M., Rojas A., Rojnokran,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I., Sodergren,E., Sonake/T., Sparks,A., Stanley,H., Stone,H., Sultan,A., Svatek/A., Tabor,P., Tameisa/A., Tamerisa,K.				

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Tang, H., Tansey, J., Taylor, C., Taylor, P., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, Y., Villalón, D., Yinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

COMMENT

Submitted (29-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced g1:17149303.

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GSKO
Center clone name: CH230-23014

COMMENT

Assembly program: Phrap; version 0.99029first call to findhaplist
Consensus quality: 134429 bases at least Q40
Consensus quality: 145218 bases at least Q30
Consensus quality: 153975 bases at least Q20
Estimated insert size: 139722; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

COMMENT

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 6106 6205: gap of unknown length
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* 11262 11361: gap of unknown length
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* 17361 17460: gap of unknown length
* 17461 23466: contig of 6006 bp in length
* 23467 23566: gap of unknown length
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* 27211 32384: contig of 5074 bp in length
* 32385 32484: gap of unknown length
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* 38099 38198: gap of unknown length
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* 46439 46538: gap of unknown length
* 46539 49455: contig of 2917 bp in length
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* 56760 56859: gap of unknown length
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* 59280 59379: gap of unknown length
* 59380 62454: contig of 3075 bp in length
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PR 16-NOV-1999: 99US-0440676.
 PR 16-NOV-1999: 99US-0440677.
 PR 29-NOV-1999: 99US-0450810.
 PR 02-DEC-1999: 99US-0453137.
 PR 08-MAR-2000: 2000US-0453137.
 XX
 PA (E0SB-) EOS BIOTECHNOLOGY INC.

XX Mack D, Gish KC;
 XX WPI: 2000-638216/61.
 DR P-PSDB: AAB00190.

PT Screening drug candidates for their ability to modulate breast cancer
 by contacting the drug to a cell expressing an expression profile gene
 and determining modulation of expression of the gene

XX
 PS Disclosure: Fig 46A-D; 258pp; English.

XX
 CC New methods for screening drug candidates are described which
 comprise adding a drug candidate to a cell that expresses a protein
 selected from BCL1, BCL2, BCL7, BCLN1, BCLN5, BCLN2, BCLN3, BCLN4
 and BCLN5 or their fragments and determining the effect of the drug
 on the expression of those proteins. Antibodies to breast cancer
 genes (specifically BCL1 or its fragment (BCL1p1 or BCL1p2)) are
 useful for inhibiting and treating breast cancer in individuals who
 are non-responsive to anti-estrogen and positive for estrogen
 receptor. Compositions comprising BCL1 or a nucleic acid encoding
 BCL1 are useful for eliciting an immune response in an individual.
 The antibodies are also useful for the diagnosis and prognosis of
 breast cancer and for screening compositions which modulate the
 breast cancer phenotype. The method allows rapid and simple
 detection of lymph node metastases.

XX
 SQ Sequence 10320 BP; 3174 A; 2005 C; 2096 G; 3042 T; 3 other;

Query Match 99.6%; Score 10278.2; DB 21; Length 10320;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 10309; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

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Db 2641 actcatgtaccaatgtatgtatttattcccaatggaaagaagatttcccgacacatac 2700
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3721 tggatatcccaaaagatgacacacttgcacatctcagataaaagttcccaagaaagta 3780
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OY 3775 ctggagatccagaatagtatcatcgtatcgttaagggagaaaggaagtcttgcgagagagca 3834
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Db 3781 ctggagatccagaataatgattccacccgtatctcgtgaaggaagaggtcttcggaagagca 3840
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QY	7255	ttggaacaatacatcatcatctctcttggaacattatgatgctgctgaacttttgataaat	7314
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Db	7381	tattttcattttttgcttct	7440
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QY	9895	gttccatttctactacaacaagcttctctgtgtgtatcttcttatgtcaacaacatcttcagca	9954
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QY	9955	gcaaaatgtctgttaacttaacttgaataataaagttttccacacagttacaacataa	10014
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QY	10015	cgagcgtttgtagtlttataatgattcattccattccctctcttagcaatagggaaatacag	10074
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Db 10320 a 10320

RESULT 2

AAC74759

ID AAC74759 standard; CDNA; 10319 BP.

XX AAC74759;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF314 polynucleotide sequence SEQ ID NO:627.

DE

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CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,

CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance

CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 10319 BP; 3176 A; 2006 C; 2093 G; 3043 T; 1 other;

Query Match 99.4%; Score 10255; DB 21; Length 10319;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 10300; Conservative 0; Mismatches 12; Indels 9; Gaps 3;

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ID ABR14485 standard; DNA; 10246 BP.
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AC ABR14485;
XX
DT 23-JAN-2002 (first entry)
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DE Human nervous system related polynucleotide SEQ ID NO 6816.
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KW Human; nootropic; neuroprotective; cytosolic; dermatological; virologic;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischistosomal; antianaemic; antiarthritic; cancer;
KW antileukemic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucifer; anticonvulsant; antitumoral;
KW antiparasitic; cardian; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
PN NO200159063-A2.
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PD 16-AUG-2001.
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PF 17-JAN-2001; 2001MO-US01334.
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 PR 05-JAN-2001: 2001US-0259678.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SK;
 XX
 DR WPI: 2001-541565/60.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,

PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure; SEQ ID NO 6816; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABA1678-ABA18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 10246 BP; 3384 A; 1827 C; 1730 G; 3305 T; 0 other;
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XX antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
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QY	5102	caacgtctgtttttcccaagccctgcctctgaatacacatgcacacccctctgtatatttt	5161
Db	4999	CACGGCTGTTTTTATCCAGGCCCTGCCTGTACATPACACATGCACACCCCTCTGTAAATTTTT	4960
QY	5162	gtcccttagatgcttcaaaactcagctagctctctgtttgttggtttgatattctctc	5221
Db	4939	GTCCCTTAGATGTTCAAAATCTACGTAGTCTCTTGTGTGGGGTTTGGATTCATTTTGTGC	4880
QY	5222	cacacatgtaaccatttttaaaaaacaatgctccgatgtctctctgttagtaattcaattta	5281
Db	4879	CACACATGTACCCCATTTTTAAAAACATGTTCCTGCATGCTCTGTATGTATTTCAATTTTA	4820
QY	5282	gcacagatctttcttctctgtctgtctgtatgaaccaagatagattgctttcttaagccctc	5341
Db	4819	GCACAGATTTCTTCTCTCTGTGTGATGAACACGATGTGATTTGCTTTCTTAAGCTCTCT	4760
QY	5342	gttggttaacaaatcccaactctgtgacatattaaactaaagaatccctcaattcaaaaga	5401
Db	4759	GTGTGTTACTAATCTCATCTTGGCAGCATTTAACTTAAGAGATTCCTCATTTCAAAACCA	4700
QY	5402	taagtgtatacaaatgtaacagcgttggttttaattgtttagaacaatgycattcttc	5461
Db	4699	TAGATGTGATACAAATCTGACCGCTGGGTTTAATTTTGATGAACACATGCGATTTCTTC	4640
QY	5462	acaaggtaaacccgcgtctatttattttttcttttggttcaataataatcccaacttgg	5521
Db	4639	ACAAGGTAACTCTGCTGTAATTTATTTTCTTTTGGTTAAATATATTTTCCAAACTTTCG	4580
QY	5522	tgctcagcagcgcgttaaggttgcgttacaacaagcgtgaagttgtataatgtaaccgc	5581
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QY	5582	aatccctcatataatgtatacaagatttagttaaagtaacatlaabagattctttagaag	5641
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QY	5642	latgctctatagaacttttaacttaagccttctgtaaaaactatcattgaagggagaag	5701
Db	4459	TATCTCTCATTAAGAACTTTTAAATCTTAAGCCTTTGTAATAACTTTCATGATAAGCAAG	4400
QY	5702	ctctcagataactgctgcaggaataagggctaaactgaactgaacttaataatttggt	5761
Db	4399	CTCTCAGCATTAACGCTCAGGGAAATAGGGCTAAATTAACGTAACTTAATTAATTTGGTT	4340
QY	5762	aaaggtgctgttaatcgagccttaatgctctgtcacaagaagtatgtaacaagctgact	5821
Db	4339	AAAGGTGCTGTATTCAGAGCTTCATAGCTTCTCTCAAGAGATGTATGTACAAAGACGTACT	4280
QY	5822	ltaataatttgcattatattgtcccaacagtaatttttttggccacggagatgtaga	5881
Db	4279	TTAATAATTTTGCAATTATATTGTGCCAACCACTAGCTTATTTATTTTGGCCACGAGATGTAGA	4220
QY	5882	agatattcaagctactgtagtgcactgtgcagataaactatttcaatnaagaagtggga	5941
Db	4219	AGATATTTCAGAGCTACTGAGTGCACACTGTGCATTAATTAATTTCATTAAAGAACTTGGGA	4160
QY	5942	gaacaataggaataaaaaaactttcttctcagtaaatatbaatgfatattacattcaaa	6001
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Db	4099	TAAATGTGCTCGACATATTGAATTAATTAATTTTCTACAGTGTACGTATAGCAACAAGATAT	4040
QY	6062	tcacatcatgcaattagctcagttctgtgcctgcctgacgttttaccatttccaatgtgc	6121
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Db	3379	AAACAAGATGAAGCAACATTTCTGATGCGATGAGATTCCTTTGGTGCTGGTG	3920
QY	6182	tgccttaagattgtaacgcgttaacaigaacaalgaagatcctgtcctataatgctag	6241
Db	3319	TGCATTAAATGTGTAAAGCGATACATGAACAATGAAAGATCTGCTGATTAAGTATGG	3866
QY	6242	aaaacaagaaggaaatgaaaatattttatagcctacttagaanaaaagggtgaccta	6301
Db	3859	AAAACAAGAAAGCAATGAAATATTTTTTAAAGCCCTACTAGGAAAAAAGGTGACCTTA	3800
QY	6302	ttcatccaagfaccttttttttttaattttaagcccttaactaactatgctatgctc	6361
Db	3799	TTCAATTCGAAGTACTTTTTTTTTTAAATTTTAAAGCTTAACTTGAATGATGCTT	3740
QY	6362	aagatataacaatatatcctcttttaattgctttgtcctatgcttctatagaacattc	6421
Db	3739	AAAGATATAAACATATATCCCTCTTTATTTGCTTGCTGATGTTCAATAGAAACATTC	3680
QY	6422	agaatatatttgaaagaatgctggaatcctgcgaacgtcat- tttttttgcatctg	6480
Db	3679	AGAAATTAATTTGATTAAGTGTGTGTGGAATCGCAACCCCTGATTTTTTTCATCTCG	3620
QY	6481	taagcatttgcactccatctttatcaatatttcgcagtgcttttgatcattgctttgt	6540
Db	3619	TATCTGCATTTCGACCTCATTTTTTACATTAAATTCGCAATTCCTTTGTATCATGTCTTTGT	3560
QY	6541	ttgggttttggtttctttttcaagtgccgggtccttggcttlaaagttagatggcaggt	6600
Db	3559	TTGGGTGTGTTTCTTTTTCACAGTCCGGGCTCTGTTCTTTAAAGTTCGATGGCAGT	3500
QY	6601	agagttcaaccaagcttgagctgctgtgttagcgatgaagttaaaaaatgcttctgctg	6660
Db	3499	AGAGTTCAACCAAGTCTGTGCTGTGTGTGACCAAGAAAGTTAAAAAATCTCTTCTCATG	3440
QY	6661	tctgtgtgcatcttcaatttttgcatttttttggctcattataaaaaaggaaaagag	6720
Db	3439	TTCTGTGTCTATTTTCATTTTTCGATTTTTCCTTTCGATTAATTAATAAAGGAAAAAGG	3380
QY	6721	aaagcaagaagcagaatcaggactaagtcctctgcttcaagttcatttgcttlaagggcct	6780
Db	3379	AAAGCAAAAGCAAAATCCAGGACGTACCTCTGCTTCAGTTTCATTTTAAGGGGCT	3320
QY	6781	tattctgctcaacctgtcgctgacttaattctcaataaactgaaaataagaagctg	6840
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QY	6841	aattggagagctttgacatccaatlaigtatgtaatttlaacttctctcttaagaaattgat	6900
Db	3259	AATTGAGGAGCTTTGCATTCAAATTAATGTGATGTAAATTAATCTGCTTAAGCAATTTTCAT	3200
QY	6901	gattgcactccaagaatgataagccagacttgagaggtgacaataaagaatcttaaaaaa	6960
Db	3199	GGATTCGATCTCAAAATGATTAACCGACTTGAAGGAGTGCAATTAAGATCTAAAAAAGA	3140
QY	6961	gaggagattccccaacaacaataatttaatttctttagtaaaaaagataacagaaatgca	7020
Db	3139	GAGAGAGATTCGCCCAAAACAACATTTTAATTTTCTAGTAAAAAGAAATTAACAATATGA	3080
QY	7021	tctggcgaaatcctlaagcaaatatctatctatgtagactgtcttlaaactgaacaacacaga	7080
Db	3079	TCGGGCAATTCCTTAAGCAACATTAATGATGTGACCTGCTTAATTCGACCAAAACACCA	3020
QY	7081	agtttggcttaacttgggaatatagcaagatattactttttggccaataactcattaaag	7140
Db	3019	AGTTTGGTTACTTGCGCAATATATGACAAGATTAATTTTGGGCAAAACTACTCATTAAG	2960
QY	7141	caatttcttaagtgtgtcggagacaatatggttcttatttttggcatgtatgcctttt	7200
Db	2959	CAATTCTCTAGTGGTGGGACAAATAGTCTTTTATTTTGTGGCATGTATGCCCTTTT	2900

QY	7201	atcttcatacaatcttcttcttctccagacagacagtagtagacaaactagacattggaa	7260
Db	2899	atttttgcattcaattttttttttttctcagacacacatactagtagtaaacacagattggaa	2840
QY	7261	aatacatacaactcattctctggacatttaagcgcgtcactcttcttgataaatctttt	7320
Db	2839	aatcacatrtactattttcttggaaattttatggcctacactcttttttggtaatttttt	2780
QY	7321	ggatagcgttcgacagatgatctcattccactctcttattttaaattctttt	7380
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Db	2719	caatlttcttcatactatcacatacttttggtagaagaaggtttggccttttgaa	2660
QY	7441	gagcacaataattatatacaacacacacccctcttcttgacataattaaagcccttacc	7500
Db	2659	gagcacaataattatatacaacacacacccctcttcttgacataattaaagcccttacc	2600
QY	7501	catctccagatatactatataaattatcttttcttaacttaagattcttgaattcttta	7560
Db	2599	catctccagatatactatataaattatcttttcttaacttaagattcttgaattcttta	2540
QY	7561	tcctaaacttggattttaaagcagactattatgtagcagaaactttttaaaggaattt	7620
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Db	2179	caagctatctagagaaagagacagcctcctaattgataactcgttagtctcaaaaggaaga	2120
QY	7981	gctgcgccactctcctcactacatacagatcttagagattttttttaaactctttagag	8040
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QY	8041	tgaatgtctgtctaaactgtctgtttagttagaggttagaatttataaagaagaagt	8100
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Db	1999	ggagatctcttctcaagtaataltaatgagaaggaaaaaaglaactctttaaagctcttc	1940
QY	8161	gttgaagccgttggtagcaattatgattataattggaactgtgaacataatcattatg	8220
Db	1939	gttgaagccgttggtagcaattatgattataattggaactgtgaacataatcattatg	1880
QY	8221	atccaagtgcgaatacagctcccaaaaatactaaatgtatataattttaaagtgcctgaag	8280
Db	1879	atccaagtgcgaatacagctcccaaaaatactaaatgtatataattttaaagtgcctgaag	1820
QY	8281	aaatacaatcttcttctaataactgaagagctcagtagtgcctattaaataatcttagg	8340

[illegible]

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PR	02-MAR-2000; 2000US-0186350
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PR	18-APR-2000; 2000US-0198123
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PR	01-SEP-2000; 2000US-0229287
PR	01-SEP-2000; 2000US-0229343
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PR	05-SEP-2000; 2000US-0229509
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PR	14-SEP-2000; 2000US-0232401
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PR	29-SEP-2000; 2000US-0236367

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
xx cancers and metastases -
PS Disclosures; SEQ ID NO 6815; 1701pp + Sequence Listing; English.
XX

The invention relates to novel genes (ABA11004-ABA21534) and proteins (AB11678-AB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; and CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 5825 BP; 1856 A; 1120 C; 1006 G; 1843 T; 0 other;

	Query Match	Best Local Similarity	Score 5793;	DB 22;	Length 5825;
			Pct Identity 99.98;	Pct Ident 0;	Mismatches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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DB	5345 AAAGTACACATACCACTTTTGGACTTCCCTTTTGACATAATGACCTTCAGAGTGAAC				5286
QY	3962 tgattgctcgcggttlcttgaglaataataagctctccgtcccttggaatccgcacact				4021
DB	5285 TGATTGGCTCGGTTCTTGAGATTAATTAAGCTCTCCCTCTGGAGAAATCCGATATTCCTTTC				5206

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Db	5225	GAATCAACGGCTGGCTGGCTACCAAACTCTGGCCAAACCTATGAGCTTATCCACCTTGA	5166
QY	4082	tcgcctccctcatcttttcaagctggttgatcaagcaatgatcatctcttagatttggcat	4141
Db	5165	TCGCTCCTCTATTTTTCAGCTGTGTGATCGACATGTGACATTCCTCTAGATTGTGGCAT	5106
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Db	4805	GAACAATGTCCAAAGTGGAAAAAATGTGAAAACCTTAAGTAAGTAACCTTAAGCAATTA	4746
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QY	4622	ttatctctcttttbatagtaggtttaccaaatataaaagtgagttaaatgataatgata	4681
Db	4625	TTATCTCTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4566
QY	4682	gaaagaatggaaagtgtlaaacacatcacttlttaaacctgttlaagttcaaacacacttg	4741
Db	4565	GAAAGATGTGAAGATGTGTAACCAATCACTTTTAAACCGTTAATGATCAAAACATTTT	4506
QY	4742	gctaataatctactggtggaataatccatagagatatccacagactagaataataatatt	4801
Db	4505	GCTAATAATGTAAGTGGGAAATTAATTCATATAGATATCACACAGATCAATTAATATAT	4446
QY	4802	lataaagaagagacacaaactgtcagaaattgaagggtttaactatattactactaa	4861
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Db	4385	AGCAAGTACGTGACCGGCATATGGACATTTGTCTCAAAACCCATTAATTTGTGCTTAAT	4326
QY	4922	tttaataatcatgaacacacttggaagggggagggggaattgaagttccaggggaattga	4981
Db	4325	TTTATATGATCATTAACCCCTTATGGCAAGAGGAGGAGAAATGTAAGGTCCAGGGCAATGA	4266
QY	4982	gaaaaatggggccctccaatcttagtctctctcatatggcatggtttagattttagact	5041
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Db	4085	gttcctttgagatgttcaaatctacagagacgtttgtgtttggcggtttacattcattttgtc	4022
QY	5222	caacatbtaccgctttttaaaaaaacaatgctccgatgctctgtagtgatcattcaatta	5281
Db	4025	CAACATATACCCCAATTTTAAATAAACATGCTCTGAGAGCTCTGTAGATTTCAATTTTA	3966
QY	5282	gccaggtattctctctcttggtgtgtatgaacacgaatgatgattggcttcttcgaagctcct	534
Db	3965	GCACAGATTTCTTCTTCTGTGTGTATACACCAATATGCAATTTGCTTTTCAACCCCTCT	3907
QY	5342	gtttgtttacaaatcctcactgttgcacattataacaaaggaatccccctaaattcaaaagca	5402
Db	3905	GTGTGTTATCAATACCTCACTTGGCACTATATACATTAAGAAAGATCCCTCAATTCAAAGCA	384
QY	5402	tagatgatacaaatgtcagacacgggtttaatttggcttagaacaatgycattctctc	5461
Db	3845	TGATGATATACCAATATGTCAAGACCGGGATTAAATTTGTTTAAACACATGGCAATTTCTTC	3788
QY	5462	acaaggtaacctcgttatcttaattcttcttggttaaatataattccaaacttgc	5521
Db	3785	ACAAGGTAAACCTGCTGTAATTTATTTATTTCTTGGTTAAATTAATTTCCAAACTTTTG	3726
QY	5522	tgatcaagcagcgtctaaagtgtaagttacaacagacatgcagttgatagtaccagcc	5581
Db	3725	TGTGTACGACGCTCTTAAGATTAGCTTACACACAGACTGCACATTTGGTAATGTACACAGCC	3666
QY	5582	aatccctctaaatgatacaagatttagttaaagatataatgattccttagaag	5641
Db	3665	AATCCCTTCAATTAANGATACATTTAGTTAAGTACATTAATAATGAGATCTTTTAGAG	3606
QY	5642	tatgtcctcagaactttaatactaaactgaagcttgttaaaacatctccgaaggaaag	5701
Db	3605	TATGTCTCTCAATACCTTTTATTAATCTTAAGCGCTTTGTAAACATATACATGAAGGAAG	3546
QY	5702	ctctcagacctaagcgtcgaaggaaatagggtcctaaataacgaaatlaaataatlggt	5761
Db	3545	CTCTCTCAGCATTAATCTGCTCAAGGAAATAGGCGCTTAATTAACGAACATTAATAATTTGGTT	3486
QY	5762	aaagtgctgttagtcgagcctcaatgcttgcataaagatgatactgacaaagactgcct	5821
Db	3485	AAAAGTGCTGTAGTCGAGCCTCAATGCTTGGCTACAAGAGATGATGACAGAGCTGACT	3426
QY	5822	ttaataattgcattatattgtcccaacacagtaattatcttttgcacaggaatgtaga	5881
Db	3425	TTAATTAATTTGCATTAATATATGTCTCCACACAGTAGTTATATTTTTCACCGAGATGTGAGA	3366
QY	5882	agatattacaagctacttgatgacacgtcagaattiaactattcaatlaaagaagtgtga	5941
Db	3365	AGATATTTAACACCTACTGTGATGACATGCAATGAGATTACTTATTTCAATTAAGAAGTTGGGA	3306
QY	5942	gaacaaatgggaaaaaaaacttaatttcttagtaaatataatgattataacttcaaa	6001
Db	3305	GAACAAATATGAAAAAAAACACTATTTTCTTAGTAATATTAATTAATTAATTCATTCATAA	3246
QY	6002	taatgtgtccctgacaatactaaataattatttctaagtgtaagtaataagaaagatat	6061
Db	3245	TAAATGTGCTGACATTAATTAATAATTAATTTCTACAGTGTAAGTAATGCAAAAGAAATAT	3186
QY	6062	lccatcatgaactgaagtcagttcttggtcctctgactgaactglttlaacatttgcacaatgtacg	6121
Db	3185	TCCATCATGACATTTAGACTCAAGTTCTTGCGCTGTGCTAGCTGTTTACAAATTTGCAAAATGTAGC	3126
QY	6122	aaacaaggtaaatgaagaacattttctcttgacgtatgataatccctttgtgtgtgtgtg	6181
Db	3125	AAACAAGGTATATGAGCAACTATATTTCTATTCACATTAATATCCCTTTGTGTGTGTGTG	3066
QY	6182	tgcattaagttgttaacggttaacatgaacaaatgaagttctctgtcataatgtatag	6241

Db	3065	TGCATTAAACTGTCTAACGGCTAACATGAAACAAATGAAAGTTCTTGGCTAATATGATGAC	3006
QY	6242	aaacaagaagaagaaatgaaatatattatgctacttaaggaaaaaaggtagaccta	6301
Db	3005	AAACAAGAAGAAATGAAATATTATTATGCGTACTTAGGAAAAAAGGTAGCCTTA	2946
QY	6302	ttctatccaaagtaactttttttttttaatttaagtccttaactacatgtaagctt	6361
Db	2945	TTCAATGCCAGTACTTTTTTTTTTAAATTTTAAAGTCCTTAATCTCATGTGTATGCTT	2866
QY	6362	aagatataaacatataaccctttttatttgcttgctatagttctataagaacattc	6421
Db	2865	AAGATGATTAACATATATCCCTTTTATTTGGCTTTGTGTATGTTTCAATGAAACATTC	2826
QY	6422	agaaattatttctgaataagctgtgtcgtgaacatcgaaacgtgaat-tttttttgacttg	6480
Db	2825	AGAAATTTATTGTAATAATGTGTGTGATGATCGACACGCTATGTTTTTTTGCATCTG	2766
QY	6481	tagtgcattctgcactccatctttaacttaatttcgaatgtgcattgtatcaattgctt	6540
Db	2765	TAGTCGCAATTTTCACCTCCATCTTAAATTAATTCGCAATGCTTCTTGTATCATGTTTGT	2706
QY	6541	tttggttttgttcttttttaagaagtcggagtccttcgcttttctaagattgtagtcagct	6600
Db	2705	TTGGGTTTTGTTCTCTTTTTCACACGTGCGCGCTTCGCTTTTAAAGTTGAGATGCGACGT	2646
QY	6601	agagttcaaacagcttcgtgactgttgtagcgaatgaattaaaaaatctcttcgtg	6660
Db	2645	AGAGTTCAACGAGTCTGAGACTGTGTACGGAATGAATTAATAAATATGCTTTTGTGATG	2586
QY	6661	tttgtttgtcaatttcaatttttgcattttttgtttgcataataaaaaagaagaagag	6720
Db	2585	TTGTGTTGCATTTTCATTTTTCGATTTTGTGTCATTTTAAATAAGAAAGAAAGAG	2526
QY	6721	aaagcaagaagacaagaataatcaggacaaagtcacccctgcgttcagttcatgttaagcgct	6780
Db	2525	AAAGCAAGAGAGAGAAATCGAGACTAGTCCCTGCTTCGATTTGCAATTTTAAACGGCGCT	2466
QY	6781	taltctgactacacgttcgcgtagctcctaataatcatcaataaactgaataaagaagatg	6840
Db	2465	TATTGTATGATCACCTGTGCGTAGCTGATATATTCATATTCATTAATTAAGATGG	2406
QY	6841	aatgaggagccttgacaatcaataatgtagatgaatttactcttccttaggaatttgat	6900
Db	2405	AATGAGAGAGCTTTGACATTTCAATTTATGATGATGATTTATTTCTCTGTAGAAATTTGAT	2346
QY	6901	gagatgcactaaagtataagcggagacttgagaggtagaactaaagaatcaaaaaa	6960
Db	2345	GGAATGCATCTCAAAATATTATAGCCAGACTGTAGAGGTGAGCAATTTAAAGTCTCAAAAAAGA	2286
QY	6961	gaagagatctccccaacaacaacatallaaatttcttagtaaaaaagaataacagaatgca	7020
Db	2285	GAGAGAGATTCCTCCCAACAACAATATTATTTCTTAGTAAAAAATAATACAGATGCA	2226
QY	7021	tctgtgcacatcccttaagcaacattatctatgttgcactgccttaaatcgaacaaacacaga	7080
Db	2225	TCTGTGCATCTTTAAACCAACATTTATCATGTGACGCTTAAATCAGCAAAACACAGA	2166
QY	7081	agtttgggttaacttgggccaataagcaagatctactcttttgggccaacactcactaataag	7140
Db	2165	AGTTTGGTTAACTTTGGCAATATGACAAGTATTTACTTTTGGCAAAAACCTCATTTAAG	2106
QY	7141	caatttctctagtgctgcgacaacaaataagttcttattatttggcattgtagtcctttt	7200
Db	2105	CAATTTCCTAGTGTGTGCGACCAAAATAGGTTCTTTATTTTGGCATTGTATGGCTTTT	2046
QY	7201	atttctcaatatttttttttttctcagacagacagataglatcaactagactgagaa	7260
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QY	7261	aataaataataactattcttggaataattatagtcagatcactcttttagtaaatatttt	7320
Db	1985	AATACATATCATCTTTCTTGGAAATTTTATATGCTCAGTCACTTTTATATGAATATTTT	1926

QY	7321	ggatagcgtttgacagatagabcttattccatacttcttattctatcttgaaatttattctt	7380
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QY	7381	catcttttgcttcatattatatacaatcttctgtgtgagaaaggttggccttttga	7440
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QY	7441	gagacaaaattatatacaacccaacccctcttcttgacatataaagcccttattc	7500
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QY	7501	catctccaagatataataataattattcttctttaaacttaagacttctcaattatta	7560
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QY	7561	ctctaaatttgtatattttaaocgagcattatgttacggaactttttaaagaattc	7620
Db	1685	ctctaaatttgtatattttaaocgagcattatgtgtacggaactttttaaagaattc	1626
QY	7621	calbatattttaggaattctctctcttggaagaagcttcccttctgtgaaatgtctgtg	7680
Db	1625	calbatattttaggaatttctctctcttggaagaagcttcccttctgtgaaatgtctgtg	1566
QY	7681	ccagctaaatctgtgtgcacattaaacaactgaaatattttaaattattgtctaat	7740
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QY	7741	ctaatttggcgtttggatccaacttttaggcggagacagcctatgcttccattcttc	7800
Db	1505	ctaatttggcgtttggatccaacttttaggcggagacagcctatgcttccattcttc	1446
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Db	1445	tttttccaactcttcttccaactccaactcccttgatattctcttcttggatlagaa	1386
QY	7861	aaccataaagagccaacccatctccgaagcgtttgtgatttggatgagagacatacagactc	7920
Db	1385	aaccataaagagccaacccatctccgaagcgtttgtgatttggatgagagacatacagactc	1326
QY	7921	caagctatagagaaaaagagacagcgtctctaatgtataactctgtatgttcaaaagaaaga	7980
Db	1325	caagctatagagaaaaagagacagcgtctctaatgtataactctgtatgttcaaaagaaaga	1266
QY	7981	gtagcccaactctctccaactgacaatcttgagattttttttaaactttaaagatag	8040
Db	1265	gtagcccaactctctccaactgacaatcttgagattttttttaaactttaaagatag	1206
QY	8041	tgtatgtctgttctaaactgtcttctgtttagtgaagtgagatttctataaaacaagactg	8100
Db	1205	tgtatgtctgttctaaactgtcttctgtttagtgaagtgagatttctataaaacaagactg	1146
QY	8101	ggatattcctttcttaagtaattataatgagaagggaaaaaagatatacttaacagctctt	8160
Db	1145	ggatattcctttcttaagtaattataatgagaagggaaaaaagatatacttaacagctctt	1086
QY	8161	gttgaagccgttggbaagacattatbtataatgtgacatgfcgacataactatattg	8220
Db	1085	gttgaagccgttggbaagacattatbtataatgtgacatgfcgacataactatattg	1026
QY	8221	atccaatgcaataagcgtcccaaaaatactaaatgtatataattttaaagcctggag	8280
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QY	8341	ctcccgcttctgtgtctcaaaaatacaaaagtacacggctcgtgagactctgtaacgtct	8400
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QY 8401 gccctgttagtaataataatgaatcattctcagaagggaatactgcacagctgg 8460
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 845 GCGCTGTTAGTAAATAAATAATGCAATTCAGAGGGGGAATATCGCATCACTGG 786
 QY 8461 tggaaatgtgaaagaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8520
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 QY 8580 aaaaaaagaagaaagaagctgcgtctgtgtgtgtgtgtgtgtgtgtgtgt 8639
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 Db 665 AAAAAAAGAAAAAAGATCAAGTCGCTCTTGTGTGTGTGTGTGTGTGTGTGT 606
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 Db 545 ATTCTATCAAAAGTAGTACTGTAGTGTGAATCTATCAAGCAAGCACTGCAAT 486
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 QY 8880 gtltcatagaagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8939
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 Db 305 CAGTTATTTGCAAGTAAATTAAGTCTGTGAATCTGTGAAGGCAAGATATGCA 246
 QY 9000 tcaatagaagaataatgtgaatcaagaatcaagaatcaagaatcaagaatgt 9059
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 QY 9120 agaaaaagaagaataactcagcgtgtgaataatgtgtgtgtgtgtgtgtgt 9179
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 Db ||||||
 Db 5 TTTT 1
 RESULT 7
 AAH13738
 ID AAH13738 standard; cDNA; 2596 BP.
 AC AAH13738;
 XX
 XX 26-JUN-2001 (first entry)
 DE Human cDNA sequence SEQ ID NO:10639.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.
 XX
 PN EPI074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000HP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 PR
 PR Primer sets for synthesizing polynucleotides, particularly the 5602
 PR full-length cDNAs defined in the specification, and for the detection
 PR and/or diagnosis of the abnormality of the proteins encoded by the
 PR full-length cDNAs -
 PS Claim 8; SEQ ID 10639; 2537pp + CD ROM; English.
 CC
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 3'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 SQ Sequence 2596 BP; 805 A; 609 C; 615 G; 567 T; 0 other;
 Query Match 24.1%; Score 2486.4; DB 22; Length 2596;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2498; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 2107 cagaagagagacacatcaccaagacagaagagctgagtggtgttaagaagagct 2166
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 Db 97 cagaagagagacacatcaccaagacagaagagctgagtggtgttaagaagagct 156
 QY 2167 tctcagaagaagagcgaggaataatgtglaagagactaatacttcagttctgtgct 2226
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 2347 gacttgcagcccgagaaagacacttgggagaaataactatccggttgcctttagaanaa 2406
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Db 337 gacttgcagcccgagaaagacacttgggagaaataactatccggttgcctttagaanaa 396
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QY 2407 gtaattgtcccaactgttcaactctgtctctcacttctcccggtgggagcgtggaagct 2466
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Db 397 gtaattgtcccaactgttcaactctgtctctcacttctcccggtgggagcgtggaagct 456
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Db 457 cgcgagtaacaacatgaatgacatcagtgatctatcaacacccctgagatgatactcc 516
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Db 517 tcttactatgaaagtgatcatgagtcaccaagcatcgatgtcaaaagaagaacatc 576
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QY 2587 acctgaaagatcgatgggagcagatctgtcaagaagaagaagaacatcattatcca 2646
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Db 577 acctgaaagatcgatgggagcagatctgtcaagaagaagaagaacatcattatcca 636
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Db 697 gctgtacaaaatgctgagtgagtttatacgttcgcgatactacatactgagc 756
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QY 2767 acttcaaacatgttcaactgtcgaagaacagacatacactacagcccggaagagagc 2826
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QY 2827 gtcalgcatatccacatcaagaagagcccaaatgtacttcaaggtctcaactgc 2886
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QY 2887 taactccagactctaaaatgggagagcaggttcttgagagtggtggaagagagagagc 2946
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QY 3307 gaggtccgggttttttggctcacaatgtcctgacccaagaagccctctctgagagagata 3366
| | | | |
Db 1297 gaggtccgggttttttggctcacaatgtcctgacccaagaagccctctctgagagagata 1356
| | | | |
QY 3367 atgcaaatgagagagatgatatgacaacgctgtgagccttacaacagagcttcaactgacac 3426
| | | | |
Db 1357 atgcaaatgagagagatgatatgacaacgctgtgagccttacaacagagcttcaactgacac 1416
| | | | |

QY 3427 ccaggtcttaaacatctatcaaacaaacaaacggttgaagagattatgagagagagacaa 3486
| | | | |
Db 1417 ccaggtcttaaacatctatcaaacaaacaaacggttgaagagattatgagagagagacaa 1476
| | | | |
QY 3487 gaaagcgcttaacccaagagacacttcaagcttgaagcttcaacaaagcagaaggggca 3546
| | | | |
Db 1477 gaaagcgcttaacccaagagacacttcaagcttgaagcttcaacaaagcagaaggggca 1536
| | | | |
QY 3547 gcaatgagagagagatcaatggaagccgttgaagagaggggtcaagaatcalctaacg 3606
| | | | |
Db 1537 gcaatgagagagagatcaatggaagccgttgaagagaggggtcagaagatcalctaacg 1596
| | | | |
QY 3607 aaggtacaagaagagaaatccactccccaagctaaagtaaatagaaagccaggttcat 3666
| | | | |
Db 1597 aaggtacaagaagagaaatccactccccaagctaaagtaaatagaaagccaggttcat 1656
| | | | |
QY 3667 tgaataaagccattctctcagagagagcttctgtaagcccaacatcttgatattaca 3726
| | | | |
Db 1657 tgaataaagccattctctcagagagagcttctgtaagcccaacatcttgatattaca 1716
| | | | |
QY 3727 aagagatgcaaccttggacatlcagataaagaatcctcaagaaagatctgagatccag 3786
| | | | |
Db 1717 aagagatgcaaccttggacatlcagataaagaatcctcaagaaagatctgagatccag 1776
| | | | |
QY 3787 gaatatgttcatcagtatctgaagggagaaagatctctgagagagggagtcctatagaa 3846
| | | | |
Db 1777 gaatatgttcatcagtatctgaagggagaaagatctctgagagagggagtcctatagaa 1836
| | | | |
QY 3847 agtacaatgagaccttgcgaacaacccaatattatctcagcccgagagccatttgaaagt 3906
| | | | |
Db 1837 agtacaatgagaccttgcgaacaacccaatattatctcagcccgagagccatttgaaagt 1896
| | | | |
QY 3907 accaagtaacccaatttggacttcccttgtacataatgacttccaagatgaaagctgagt 3966
| | | | |
Db 1897 accaagtaacccaatttggacttcccttgtacataatgacttccaagatgaaagctgagt 1956
| | | | |
QY 3967 ggcctcggttcttggagtaataataagctctccgttccgttggaaatccgacatactgagtc 4026
| | | | |
Db 1957 ggcctcggttcttggagtaataataagctctccgttccgttggaaatccgacatactgagtc 2016
| | | | |
QY 4027 acgtgccttgcgtctcccaacatcccttgcgaacaatgagtcctatccacacttcaatcgc 4086
| | | | |
Db 2017 acgtgccttgcgtctcccaacatcccttgcgaacaatgagtcctatccacacttcaatcgc 2076
| | | | |
QY 4087 cctcccatcttccagcctgttggatccagacatgacatccctctagatlttgggagatcagc 4146
| | | | |
Db 2077 cctcccatcttccagcctgttggatccagacatgacatccctctagatlttgggagatcagc 2136
| | | | |
QY 4147 attccaagcctgggcccacactgcaaacggttgcctccaagggagaaacgaaaggacaccaa 4206
| | | | |
Db 2137 attccaagcctgggcccacactgcaaacggttgcctccaagggagaaacgaaaggacaccaa 2196
| | | | |
QY 4207 atgtlaaaaaatgaaaggtcccttgaatgtgagtaaaaaagagaaagtgtgtagaagtactc 4266
| | | | |
Db 2197 atgtlaaaaaatgaaaggtcccttgaatgtgagtaaaaaagagaaagtgtgtagaagtactc 2256
| | | | |
QY 4267 aagatgaacttcaacaaatgtgtgacatgttggacatgtcttcttctgagatgagatgt 4326
| | | | |
Db 2257 aagatgaacttcaacaaatgtgtgacatgttggacatgtcttcttctgagatgagatgt 2316
| | | | |
QY 4327 atgcttgcagatgagttgcacatgttgcagatggaacattccagtgacagatgacagc 4386
| | | | |
Db 2317 atgcttgcagatgagttgcacatgttgcagatggaacattccagtgacagatgacagc 2376
| | | | |
QY 4387 atcttgcagagcacaatatgtacttcaacaacataccagaggggcttgcataagagaca 4446
| | | | |
Db 2377 atcttgcagagcacaatatgtacttcaacaacataccagaggggcttgcataagagaca 2436
| | | | |
QY 4447 atgcacaagtgtg-aaaaaaatggaanaaccttaagagtaaaaccttaagcatttaacaaat 4505
| | | | |
Db 2437 atgcacaagtgtgaaaaaaatggaanaaccttaagagtaaaaccttaagcatttaacaaat 2496
| | | | |
QY 4506 taaatagaataggttcttcttgatggagatcaatagcttgaatgtcttatgaagaacct 4565
| | | | |

Db 2497 taatagaaataggtttcttgatcggaattcaatagcttgtaatgttcttaagaacct 2556
QY 4566 attaaaaaatactcaatagagccttgcttataccaacatg 4605
Db 2557 attaaaaaatactcaatagagccttgcttataccaacatg 2596

RESULT 8
AAD06845
ID AAD06845 standard: DNA; 2327 BP.

AC AAD06845;

DT 06-APR-2001 (first entry)

DE Human breast cancer specific gene-3 (BCSG-3) #1.

KW Human: breast cancer specific gene-3; BCSG-3; cytostatic; vaccine;
breast cancer; therapeutic; gene therapy; ds.

OS Homo sapiens.

PN M0200137779-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000MO-DS32056.

PR 23-NOV-1999; 99US-0166973.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Cafferkey R, Reclon H, Sun Y;

DR WPI; 2001-367602/38.

PT Novel breast cancer specific gene for diagnosing, monitoring, staging,
imaging, preventing and treating cancers, particularly breast cancer -
PS Claim 1; Page 50; 66pp; English.

CC The invention relates human breast cancer specific genes (BCSG's) and
their corresponding proteins. BCSG is useful for diagnosing, staging,
monitoring, imaging, preventing and treating breast cancers. BCSG is also
useful for inducing an immune response against a target cell expressing
BCSG. The invention also provide methods for detecting genetic lesions or
mutations in BCSG, thereby determining if a human with the genetic lesion
is at risk for breast cancer or has breast cancer. BCSG antibodies
labelled with paramagnetic ions or radioisotopes is useful for imaging
breast cancers, while BCSG antibodies conjugated to a cytotoxic agent is
useful for treating breast cancer. BCSG is useful in the rational design
of new therapeutics for imaging and treating cancers. BCSG is also used
in gene therapy. The present DNA sequence is human breast cancer specific
gene-3 (BCSG-3) or Gene ID 274731.

CC Sequence 2327 BP; 720 A; 371 C; 443 G; 765 T; 28 other;

Query Match 21.9%; Score 2257.6; DB 22; Length 2327;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2293; Conservative 0; Mismatches 32; Indels 3; Gaps 3;

QY 6898 gatgatgcatctcaaaatgataagcagacttgagaggtgacaattaaagatctaaaa 6957
Db 1 gatgatgcatctcaaaatgataagcagacttgagaggtgacaattaaagatctaaaa 60
QY 6958 agagagagagattcccccaaacacacatttaattttcttgataaagaataacgaat 7017
Db 61 agagagagagattcccccaaacacacatttaattttcttgataaagaataacgaat 120
QY 7018 gcatcgtggaactcttaagacattatctatgtgagctgcttaaaacgcaaacac 7077

Db 121 gcatcgtggaactcttaagacattatctatgtgagctgcttaaaacgcaaacac 180
QY 7078 agaagttgttacttggtgcaatgacaaagtattcttttggcgaacactccatt 7137
Db 181 agaagttgttacttggtgcaatgacaaagtattcttttggcgaacactccatt 240
QY 7138 aagcaattctctagtgtgtcgacacaaataggtcttatttttggcagatgacct 7197
Db 241 aagcaattctctagtgtgtcgacacaaataggtcttatttttggcagatgacct 300
QY 7198 ttatttttcaatt 7257
Db 301 ttatttttcaatt 360
QY 7258 gaaatcacatcatcttcttggaatttttgaatggttcagcttcttttgtaaatatt 7317
Db 361 gaaatcacatcatcttcttggaatttttgaatggttcagcttcttttgtaaatatt 420
QY 7318 ttggatagcgttgacagatagatcttcatcactcttatttttttttttttttttt 7377
Db 421 ttggatagcgttgacagatagatcttcatcactcttatttttttttttttttttt 480
QY 7378 ttcatatttttgcttcaattataacacattttgttgagaagaagtttggtttttg 7437
Db 481 ttcatatttttgcttcaattataacacattttgttgagaagaagtttggtttttg 540
QY 7438 aaagagacaaaatttataactaaactaaactcttttttgcatataaagcctta 7497
Db 541 aaagagacaaaatttataactaaactaaactcttttttgcatataaagcctta 600
QY 7498 ttccatctctcagatatattataaatttttttaatttaagaatttcgaatttt 7557
Db 601 ttccatctctcagatatattataaatttttttaatttaagaatttcgaatttt 660
QY 7558 ttatcttaatttgatatttaaaacgactatagtgacggaacttttttaatgagaa 7617
Db 661 ttatcttaatttgatatttaaaacgactatagtgacggaacttttttaatgagaa 720
QY 7618 ttcatgttgatttaggaattttctcttggaagaagcttcccttgatgaaatgat 7677
Db 721 ttcatgttgatttaggaattttctcttggaagaagcttcccttgatgaaatgat 780
QY 7678 gtgcagactaaactgtgtgcatttaaaactgaaataatttaaatattgttcatt 7737
Db 781 gtgcagactaaactgtgtgcatttaaaactgaaataatttaaatattgttcatt 840
QY 7738 attcaatttgagtttgatcaaaacttgagcaggaacagctatgcttccattct 7797
Db 841 attcaatttgagtttgatcaaaacttgagcaggaacagctatgcttccattct 900
QY 7798 tcccttttcaacttttctctcatcactcactcctgtatcttctgttttgatag 7857
Db 901 tcccttttcaacttttctctcatcactcactcctgtatcttctgttttgatag 960
QY 7858 aaaatcatagaagcccaaccatctcagaagcgttgatgtagagagacatcatga 7917
Db 961 aaaatcatagaagcccaaccatctcagaagcgttgatgtagagagacatcatga 1020
QY 7918 ctcaaatatagagaagaagcagagctcctaatttgtaacatcctgtagttaaaagaa 7977
Db 1021 ctcaaatatagagaagaagcagagctcctaatttgtaacatcctgtagttaaaagaa 1080
QY 7978 agagatgcccattctctctacatgacatattgagatttttttaacactttttaga 8037
Db 1081 agagatgcccattctctctacatgacatattgagatttttttaacactttttaga 1140
QY 8038 tagagatggttctgtcttaactgttcgttttagtgagagatctttataaacaagc 8097
Db 1141 tagagatggttctgtcttaactgttcgttttagtgagagatctttataaacaagc 1200
QY 8098 atggagattcttcttaagagtaatttaagaagaagaagaagaatattccttaacagctc 9157
Db 1201 atggagattcttcttaagagtaatttaagaagaagaagaagaagaatattccttaacagctc 1260

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QY 8158 ttgttgaagccgtgtgtgagcaatattgttataatgtcacaatgtgcacataatctatt 8217
DB 1261 ttgttgaagccgtgtgtgagcaatattgttataatgtcacaatgtgcacataatctatt 1320
QY 8218 atgataatgcaataatcagctcccaaaaataataatgtatataatatttaaatgtcctg 8277
DB 1321 atgataatgcaataatcagctcccaaaaataataatgtatataatatttaaatgtcctg 1380
QY 8278 aggaataacatlttcttaataacagagagctcagatagcgtatggtatataaatattt 8337
DB 1381 aggaataacatlttcttaataacagagagctcagatagcgtatggtatataaatattt 1440
QY 8338 agccctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8397
DB 1441 agccctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
QY 8398 gctgcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8457
DB 1501 gctgcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
QY 8458 tggtagaaatgtgagaaagaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8517
DB 1561 tggtagaaatgtgagaaagaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620
QY 8518 gccctaagttgagagaggttcaactttagctactgtcttgtgtgtgtgtgtgtgtgtgt 8577
DB 1621 gccctaagttgagagaggttcaactttagctactgtcttgtgtgtgtgtgtgtgtgtgt 1680
QY 8578 aaaaaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 8637
DB 1681 aaaaaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 1740
QY 8638 gactgtccaaagcacaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 8697
DB 1741 gactgtccaaagcacaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 1800
QY 8698 atattcacaatcaaaagaaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtg 8757
DB 1801 atattcacaatcaaaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 1860
QY 8758 aagaagaatagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 8817
DB 1861 aagaagaatagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1920
QY 8818 aagaagcacaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 8877
DB 1921 aagaagcacaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1980
QY 8878 ctgttcaatagacagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8937
DB 1981 ctgttcaatagacagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
QY 8938 cccagtttaattgagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgag 8997
DB 2041 cccagtttaattgagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgag 2099
QY 8998 tgtacaatgaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 9057
DB 2100 tgtacaatgaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 2159
QY 9058 acattcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 9117
DB 2160 acattcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2219
QY 9118 ggaagaaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgag 9176
DB 2220 ggaagaaagaaagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaaatgtgagaa 2279
QY 9177 tgtcctt-ctagaacatagagctcccaaaactcaattcgtgtgtgtgtgtgtgtgtgt 9223
DB 2280 tgtccttctagagatagagctcccaaaactcaattcgtgtgtgtgtgtgtgtgtgt 2327

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RESUME 9

AAH16992

ID AAH16992 standard; cDNA; 1587 bp.

XX AC AAH16992;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA sequence SEQ ID NO:16281.

XX KW Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Suyiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI: 2001-318749/34.

XX PT Primer sets for synthesizing polynucleotides, particularly the 5602

XX PT full-length cDNAs defined in the specification, and for the detection

XX PT and/or diagnosis of the abnormality of the proteins encoded by the

XX PT full-length cDNAs -

XX PS Claim 8; SEQ ID 16281; 2537bp + CD ROM; English.

XX XX The present invention describes primer sets for synthesizing 5602

XX CC full-length cDNAs defined in the specification. Where a primer set

XX CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

XX CC to the complementary strand of a polynucleotide which comprises one of

XX CC the 5602 nucleotide sequences defined in the specification, where the

XX CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

XX CC of an oligonucleotide comprising a sequence complementary to the

XX CC complementary strand of a polynucleotide which comprises a 5'-end

XX CC sequence and an oligonucleotide comprising a sequence complementary to a

XX CC polynucleotide which comprises a 3'-end sequence, where the

XX CC oligonucleotide comprises at least 15 nucleotides and the combination of

XX CC the 5'-end sequence/3'-end sequence is selected from those defined in

XX CC the specification. The primer sets can be used in antisense therapy and

XX CC in gene therapy. The primers are useful for synthesizing polynucleotides,

XX CC particularly full-length cDNAs. The primers are also useful for the

XX CC detection and/or diagnosis of the abnormality of the proteins encoded by

SQ Sequence 1587 BP; 486 A; 244 C; 276 G; 581 T; 0 other:

Query Match 15.3%; Score 1580.6; DB 22; Length 1587;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1583; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6988 taattcttagtaaaagaaataacagatgcgtgtgcaatccttaagaacataatc 7047

QY	8128	gagaaagggaaaaaagatcattcctttaaagcctctctgttgaagcctgtaggagacattatgt	8187
Db	1141	gagaaagggaaaaaagatcattcctttaaagcctctctgttgaagcctgtaggagacattatgt	1200
QY	8188	ttataattgacacttgacacttaactctatctatgatagcataatgcacaatacagctccaaaat	8247
Db	1201	ttataattgacacttgacacttaactctatctatgatagcataatgcacaatacagctccaaaat	1260
QY	8248	atttaaatgatatatattttaaagtctctgagaaatacatttctttaaataactgaag	8307
Db	1261	atttaaatgatatatattttaaagtctctgagaaatacatttctttaaataactgaag	1320
QY	8308	agctccagataagcgcatataaataatattatagccctccctgtgtgtgtgctgcaaaacatca	8367
Db	1321	agctccagataagcgcatataaataatattatagccctccctgtgtgtgtgctgcaaaacatca	1380
QY	8368	caaaagtacccggtctcttgagacacttgtaactgctgcccgttttagttaataataaattatgc	8427
Db	1381	caaaagtacccggtctcttgagacacttgtaactgctgcccgttttagttaataataaattatgc	1440
QY	8428	attctcagaaggggggaataatctgcgcatcccaagctgtgtgtggaatgtgtgagtaagaagctgtgc	8487
Db	1441	attctcagaaggggggaataatctgcgcatcccaagctgtgtgtggaatgtgtgagtaagaagctgtgc	1500
QY	8488	gtctgcctctctgtcgtatgtccagcctcttgccttaaatttgaaagagaggttcaactttgc	8547
Db	1501	gtctgcctctctgtcgtatgtccagcctcttgccttaaatttgaaagagaggttcaactttgc	1560
QY	8548	tactgtccttgccttttgagaccattgc	8574
Db	1561	tactgtccttgccttttgagaccattgc	1587

RESULT 10
AAH15234
ID AAH15234 standard; cDNA: 1551 BP.
AC AAH15234;
XX
XX
D7 26-JUN-2001 (first entry)
XX
XX
DE Human cDNA sequence SEQ ID NO:13348.
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
PN EPI074617-AZ.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
P1 Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
P1 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPL; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PM and/or diagnosis of the abnormality of the proteins encoded by the
PM full-length cDNAs -
XX

Claim 8; SEQ ID 13348; 2537bp + CD ROM; English.

Query Match	14.9%	Score 1537;	DB 22;	Length 1551;
Best Local Similarity	99.9%	Pred. No. 8.2e-315;		
Matches 1549; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 1

[illegible]

Query	Match	Similarity	9.8%;	Score 1007;	DB 21;	Length 1009;
Best local	Similarity	99.8%;	Pred. No. 7.5e-203;			
Matches 1007;	Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	7581	cgagcctatcgtacgtacgactctttttaaagaagatctcaatgatgatcttaggaattt	7640			
Db	1	cgagctattatgtacgtacgactctttttaaagaagatctcaatgatgatcttaggaattt	60			
QY	7641	cctctttggaaaagagcttccctcctgtatgaatcgtatgacgtatgcacaaattgtgtgca	7700			
Db	61	ctctcttggaaaagagcttccctcctgtatgaatcgtatgacgtatgcacaaattgtgtgca	120			
QY	7701	tttaaaacgtgaaatatttttaaattatgtgtcatatcttcaaatcgtacgttgatca	7760			
Db	121	tttaaaacgtgaaatatttttaaattatgtgtcatatcttcaaatcgtacgttgatca	180			
QY	7761	aactttaggcagagaccagctatcgtcttcacatctctcttcttaacgtcttctctca	7820			
Db	181	aactttaggcagagaccagctatcgtcttcacatctctcttcttaacgtcttctctca	240			
QY	7821	tcactacccctgtattcaatctctgttctgttgggatagaanaaaatcaataagsgccaacca	7880			
Db	241	tcactacccctgtattcaatctctgttctgttgggatagaanaaaatcaataagsgccaacca	300			
QY	7881	tctagaagctgtgtgattgttgagagagacacatacgtactccaagtatacgtagaanaagac	7940			
Db	301	tctagaagctgtgtgattgttgagagagacacatacgtactccaagtatacgtagaanaagac	360			
QY	7941	agagctctaatcgtatcaactcgtatgttccaanaagaaagatgagcccaattctctctac	8000			
Db	361	agagctctaatcgtatcaactcgtatgttccaanaagaaagatgagcccaattctctctac	420			
QY	8001	atgacatattgagatctttttttaaactcaacttttaagatagatgctcgttcttaacy	8060			
Db	421	atgacatattgagatctttttttaaactcaacttttaagatagatgctcgttcttaacy	480			

RESULT 12
 AAF44852
 ID AAF44852 standard; cDNA: 996 BP.
 XX
 AAF44852:
 XX
 28-MAR-2001 (first entry)
 DT
 XX
 Human breast cancer related protein coding sequence SPO ID NO: 8.
 DE
 XX
 Human: breast cancer; diagnosis; therapy; vaccine; ss.
 KW
 XX
 Homo sapiens.
 OS
 XX
 M0200078960-A2.
 PN
 XX
 28-DEC-2000.
 PD
 XX
 23-JUN-2000; 2000WO-US17536.
 PF
 XX
 23-JUN-1999; 99US-0140903.
 PR
 XX
 12-OCT-1999; 99US-0158980.
 PR
 XX
 (CORI-) CORIXA CORP.
 PA
 XX
 Yuguu J, Mitcham JL;
 PI
 XX
 WPI; 2001-041426/05.
 DR
 XX
 New polynucleotides encoding breast tumor specific proteins, useful for
 PT prevention, treatment and diagnosis of breast cancer -
 PP
 XX
 Claim 5; Page 120; 165pp; English.
 PS
 XX
 The present invention provides the coding sequences for a number of
 CC

D6 928 caccctgcgtgtagcttcatttccataactcgaataaaagaagcggaatvtagtgct 987
QY 6852 ttgaacatc 6860
DB 988 tttttttt ||
988 tttttttt q96

RESULT	13
AAAF82511	
ID	AAAF82511 standard: cDNA: 766 bp

Query Match	Best Local Similarity	7.4%	Score 761.4	DB 22	Length 766
Matches 762; Conservative 0; Mismatches 4; Indels 0; Gaps 0					
9243	ttcccaacatgaatgaatgacagatatacatttcttcttggctgaagttctctacc	9302			
1	tttcccaacatgaatgaatgacagatatacatttcttcttggctgaagttctctacc	60			
9303	tgtaaatgtgaataatataatgataatataatataatataatataatataatgataatg	9362			
61	tgtaaatgtgaataatataatgataatataatataatataatataatataatgataatg	120			
9363	actgtgtgtgaazagacattgagatccttggctgtgaagagacacatagagtgccaagt	9422			
121	actgtgtgtgaazagacattgagatccttggctgtgaagagacacatagagtgccaagt	180			
9423	tattatgtgagcagaggggttattttaaactgtgacgttcccaaggccaggaagtgtgg	9482			
181	tattatgtgagcagaggggttattttaaactgtgacgttcccaaggccaggaagtgtgg	760			

QY 9483 gtcaattttcttaagacagcgtgtaatactagcagcgaatagtgtaatac 9542
 Db 241 gtcaattttcttaagacagcgtgtaatactagcagcgaatagtgtaatac 300
 QY 9543 aagatgcaaaactattactagcgtgtaatactagcagcgaatagtgtaatac 9602
 Db 301 aagatgcaaaactattactagcgtgtaatactagcagcgaatagtgtaatac 360
 QY 9603 caaatacacaataaataacgcaaaatctcttagggcgactattgacacacatgga 9662
 Db 361 caaatacacaataaataacgcaaaatctcttagggcgactattgacacacatgga 420
 QY 9663 aaactttgggggagcgtgaggggagacatcacaatgccaatgtaaatlaacta 9722
 Db 421 aaactttgggggagcgtgaggggagacatcacaatgccaatgtaaatlaacta 480
 QY 9723 caagcaatttccacagcagaagaatgcttctcataaggaatgtaattcgttgaaga 9782
 Db 481 caagcaatttccacagcagaagaatgcttctcataaggaatgtaattcgttgaaga 540
 QY 9783 aagaattcaatttgatctcgtatggaatactagtaagtggtgataatagttctgtc 9842
 Db 541 aagaattcaatttgatctcgtatggaatactagtaagtggtgataatagttctgtc 600
 QY 9843 ttacaacacagaaatlttctgtttatttatttatttatttatttatttatttattt 9902
 Db 601 ttacaacacagaaatlttctgtttatttatttatttatttatttatttatttattt 660
 QY 9903 ctactcacaacatgcttctgtgtaattcttataagcaaaatctcagcagcaagaat 9962
 Db 661 ctactcacaacatgcttctgtgtaattcttataagcaaaatctcagcagcaagaat 720
 QY 9963 gctcgttaccatcttaacttgaataaagttttaccacagttac 10008
 Db 721 gctcgttaccatcttaacttgaataaagttttaccacagttac 766

RESUL 14
 ID AAH03367 standard; cDNA: 691 BP.
 AC AAH03367;
 XX
 DT 26-JUN-2001 (first entry)
 DE Human cDNA clone (5'-primer) SEQ ID NO:202.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 PN EPI074617-A2.
 PD 07-FEB-2001.
 PE 28-JUN-2000; 2000FP-0116126.
 PR 29-JUN-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WP: 2001-318749/34.
 PR Primer sets for synthesizing polynucleotides, particularly the 5602
 full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the
 PS full-length cDNAs -
 Claim 1: SEQ ID 202; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03366 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 691 BP; 211 A; 93 C; 104 G; 280 T; 3 other:

Query Match 6.6%; Score 681.6; DB 22; Length 691;
 Best Local Similarity 99.0%; Pred. No. 3.5e-134;
 Matches 684; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 1 taatttcttaagtaaaagataacagatgcatacgtgcgaatccttaagcaacattac 60
 QY 7048 tatgtgagctgcttaatacgcacaacacagaaagtttgtaactctggcgaattgaca 7107
 Db 61 tatgtgagctgcttaatacgcacaacacagaaagtttgtaactctggcgaattgaca 120
 QY 7108 agtattacttttgggcaaaactactcaataagcaattctcagtgctgcgacacaa 7167
 Db 121 agtattacttttgggcaaaactactcaataagcaattctcagtgctgcgacacaa 180
 QY 7168 taggttcttaatttggcagtcgatgcttttttatttcaatattttttttctc 7227
 Db 181 taggttcttaatttggcagtcgatgcttttttatttcaatattttttttctc 240
 QY 7228 agacagacatagtagtatacactagcattggaataacatatactactcttggaatt 7287
 Db 241 agacagacatagtagtatacactagcattggaataacatatactactcttggaatt 300
 QY 7288 tatgtgaagctactttttagtaaaataatttggatagcgttgacagatagatctat 7347
 Db 301 tatgtgaagctactttttagtaaaataatttggatagcgttgacagatagatctat 360
 QY 7348 tccactactcttattatgataatttatttcaatttttgccttcaatattatata 7407
 Db 361 tccactactcttattatgataatttatttcaatttttgccttcaatattatata 420
 QY 7408 ttgtgtgagaaagagtggtctttttgaaagagacaataattattataacacaa 7467
 Db 421 ttgtgtgagaaagagtggtctttttgaaagagacaataattattataacacaa 480
 QY 7468 cactccttttgaacatataagccttattccactctcagaatatataataatt 7527
 Db 481 cactccttttgaacatataagccttattccactctcagaatatataataatt 540
 QY 7528 atttttaattaaatttcgaattatttttcttaattgtgatttaacagacata 7587

Search completed: July 21, 2002, 21:50:11
Job time: 21033 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 15:11:53 ; Search time 168.22 seconds

(without alignments)
15061.881 Million cell updates/sec

Title: US-09-702-216-1

Percent score: 10315

Sequence: 1 ttccctccgcaagcgtcctt.....gttatttcaaaaaaaaaa 10315

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata2/ina/6A.COMB.seq:*
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6: /cgn2_6/ptodata2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.4	3.1	333	US-09-284-782-36	Sequence 36, Appl
2	72.4	0.7	19124	US-08-487-8268-13	Sequence 13, Appl
3	69.2	0.7	7218	US-08-232-463-14	Sequence 14, Appl
4	65	0.6	1456	US-09-037-135-1	Sequence 1, Appl
5	59.6	0.6	837	US-08-998-416-288	Sequence 288, App
6	59.4	0.6	2110	US-09-419-459-1	Sequence 1, Appl
7	58.8	0.6	636	US-08-998-416-1137	Sequence 1137, Ap
8	58.2	0.6	6243	US-09-056-075-1	Sequence 1, Appl
9	57.4	0.6	1004	US-08-465-590-8	Sequence 8, Appl
10	57.4	0.6	1004	US-08-283-300A-7	Sequence 7, Appl
11	57.4	0.6	1004	US-08-711-417C-8	Sequence 8, Appl
12	57.4	0.6	1004	US-08-283-300A-7	Sequence 8, Appl
13	57.4	0.6	1386	US-08-465-590-3	Sequence 3, Appl
14	57.4	0.6	1386	US-08-283-300A-2	Sequence 2, Appl
15	57.4	0.6	1386	US-08-711-417C-3	Sequence 3, Appl
16	57.4	0.6	1386	US-08-998-416-186	Sequence 186, App
17	57.4	0.6	1551	US-08-998-416-595	Sequence 595, App
18	57.4	0.6	1551	US-08-213-419B-3	Sequence 3, Appl
19	57.4	0.6	1551	US-08-213-419B-3	Sequence 3, Appl
20	56.8	0.6	19124	US-08-487-8268-13	Sequence 13, Appl
21	55.8	0.5	618	US-08-998-416-186	Sequence 186, App
22	55.6	0.5	618	US-08-998-416-186	Sequence 186, App
23	55.4	0.5	6124	US-08-213-419B-3	Sequence 3, Appl
24	54	0.5	7218	US-08-232-463-14	Sequence 14, Appl
25	53.8	0.5	2897	US-08-927-394-1	Sequence 2, Appl
26	53.2	0.5	731	US-08-451-405A-2	Sequence 4, Appl
27	52.4	0.5	3356	US-09-379-523-4	Sequence 4, Appl

28	51.2	0.5	2223	US-08-257-073-4	Sequence 4, Appl
29	50.6	0.5	1128	US-08-465-590-7	Sequence 7, Appl
30	50.6	0.5	1128	US-08-283-300A-6	Sequence 6, Appl
31	50.6	0.5	1128	US-08-711-417C-7	Sequence 7, Appl
32	50.6	0.5	1128	PCT-US95-09345-6	Sequence 6, Appl
33	50.6	0.5	1170	US-08-465-590-6	Sequence 6, Appl
34	50.6	0.5	1170	US-08-283-300A-5	Sequence 5, Appl
35	50.6	0.5	1170	US-08-711-417C-6	Sequence 6, Appl
36	50.6	0.5	1170	PCT-US95-09345-5	Sequence 5, Appl
37	50.6	0.5	1296	US-08-465-590-4	Sequence 4, Appl
38	50.6	0.5	1296	US-08-283-300A-3	Sequence 3, Appl
39	50.6	0.5	1296	US-08-711-417C-4	Sequence 4, Appl
40	50.6	0.5	1296	PCT-US95-09345-3	Sequence 3, Appl
41	50.6	0.5	1788	US-08-465-590-2	Sequence 2, Appl
42	50.6	0.5	1788	US-08-283-300A-1	Sequence 1, Appl
43	50.6	0.5	1788	US-08-711-417C-2	Sequence 2, Appl
44	50.6	0.5	1788	PCT-US93-08743-2	Sequence 2, Appl
45	50.6	0.5	1788	PCT-US95-09345-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-284-782-36
; Sequence 36, Application US/09284782
; Patent No. 6057111
; GENERAL INFORMATION:
; APPLICANT: ENTERPRISES, LTD., GBI
; APPLICANT: Deliss, Louis P.
; APPLICANT: Yehliely, Fruma
; APPLICANT: Elmova, Elena
; APPLICANT: Vasquez-Taslop, No. 6057111a C.
; APPLICANT: Elinat, Paz
; TITLE OF INVENTION: GENE IDENTIFICATION METHOD
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohli & Associates
; STREET: 30500 No. 6057111thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N
; REGISTRATION NUMBER: 38,972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-284-782-36

Query Match 3.1%; Score 315.4; DH 3; Length 333;
Best Local Similarity 99.7%; Pred. No. 1.3e-67;
Matches 316; Conservative 0; Mismatches 1; Indels 0;


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Query Match      0.73: Score 72.4; DB 2; Length 19124;
Best Local Similarity 49.08: Pred. No. 2.3e-07;
Matches 257; Conservative 0; Mismatches 256; Indels 11; Gaps 2;

QY 7060 ttaatcagaacaaacccagaagtttggttaacttgggcataatgcaagttaacttct 7119
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Db 15920 TATATCATTAATTAATTTTAAATTTTAAATTTTAAATTAATTAATTAATTAATTT 15861
QY 7120 tgggcaaaactactcctaatgaacaaattctctagttgtgcgacaacaattagttcttat 7179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15860 TTTTATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15801
QY 7180 ttgggaigtatgccttttaattcattcacaatttttttttcttcacagacaatag 7239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15800 ATTTTATGTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15749
QY 7240 tagatcaactgacattggaataacacatctcacttcttcggaaatttaagtcagct 7299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15748 TGAATATATTTTATTTTAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAA 15689
QY 7300 accttttagtaaatatatttttggatagcgttcacagatagatccttaactcacc--tt 7356
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Db 15688 TTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15629
QY 7357 cttaattatgtaattttatcttcttcttgcctcattatatacatttttggtgg 7416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15628 TTTTATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15569
QY 7417 agaagaggttggccttttgcgaagsgacaaaattatataaacacacacccctt 7476
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Db 15568 ATCAAAATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15509
QY 7477 ttgcacatactaaagcccttatccatctcctcaagatataataaattatattttta 7536
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15508 TTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15449
QY 7537 attaaattcttgcaattatattatcttaactaaatttgtatttaaa 7580
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Db 15448 TTAATTAATTTGTTTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15405

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300, 6
; FILING DATE: 26-AUG-1991

```

7161 acacgaataggtccttatttttggcatgatgccttttatttcattcaatttttt 7220
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 Db 6 AAATATATATTAATTATTAATAAGATTAATAACCTTTTATATATATTTAAGT 65

QY 7221 ttcttcagacagacatagtagtatacactagcattggaaaatacatacactatcttg 7280
DB 66 ATTAAATATTATTAACATATTATCATATTATTAATAATTAATTAATTAATTAATA 125
QY 7281 gaattatagtgtagcactccttttaagaaaatacttttgtagcgttgacagatag 7340
DB 126 CTTATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 185
QY 7341 aactatccactccttcttattatgataattatcttaacttttgccttccatctat 7400
DB 186 TAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 245
QY 7401 atacatcttgcgtggaagaggttggtgcttttgaagagacaaaattatctaa 7460
DB 246 AAAATATTATTAGATTATTATTATTCTTTAATAAATTAAATGATTATCACTAAT 305
QY 7461 cactaacaccccttttgacctatcaagcctttatccactcccaagatatatat 7520
DB 306 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 365
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DB 366 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 425
QY 7581 cgaactatagtgacggaactttcttaacggaattcatgattgagattt 7640
DB 426 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 485
QY 7641 ctctctggaagagctcccttgtagaagaatgagtgccgcaaatgtgagcca 7700
DB 486 TTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 545
QY 7701 tttaaaacigaaaatattttaaattatcttatacttcaaat 7746
DB 546 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 591

RESULT 6

US-09-419-459-1/c
; Sequence 1137, Application US/09419459
; Patent No. 6222028
; GENERAL INFORMATION:
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Tsai, Cheng-Fang
; APPLICANT: Chang, Chia-Chieh
; TITLE OF INVENTION: CELLULOSE ENZYMES
; FILE REFERENCE: 08919/037001
; CURRENT APPLICATION NUMBER: US/09/419,459
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Piomyces rhizinflata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1749)
US-09-419-459-1

Query Match 0.6%; Score 59.4; DB 4; Length 2110;
Best Local Similarity 49.9%; Pred. No. 0.0001;
Matches 202; Conservative 0; Mismatches 201; Indels 2; Gaps 2;

QY 7167 atagttcttatttgtagcagtagcctttatctcaatctttttctct 7226
DB 2108 ATTATTTTATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2049
QY 7227 cagacagacatagtagtatacactagcattggaaaatacatacactatcttgagatat 7286

DB 2048 ACAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1990
QY 7287 ttatgtagcagtagccttttgaagaaaatttttgtagagcgttgacagatagactta 7346
DB 1989 TTGATTTTAAATTAATTTCTTTTTCCTTTAAGTAAGAAAGTAATTAATTAATTAAT 1930
QY 7247 ttccactccttattatgataattatcttaacttttgccttccatctatctat 7406
DB 1929 TTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1870
QY 7407 atttgtagaagaggttggtgcttttgaagagcaaaaattatatacactaa 7466
DB 1869 AATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1811
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DB 1810 TATTATTATTTTAAATTAATTTTCAATTAAGAAATTTATTTCTTTATTAATTAAT 1751
QY 7527 tatctttaaactgaattctgaattatcttccatcttaattgt 7571
DB 1750 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1706

RESULT 7

US-08-998-416-1137
; Sequence 1137, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtel, Philipp
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYP11
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigis, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PR/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1692RP

RESULT 10
US-08-283300A-7
Sequence 7, Application US/08283300A
Patent No. 6172278
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,300A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438

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APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENC/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1386
? US-08-465-590-3

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Best Local Similarity 60.6%; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtcactgtgacatgtcttcttgatgaagatgatagtatgttcataatagt 4343
DB 1213 AAGTGGCAACACTGCCGGGTGCTCTTCCTGGATCAGTCATGTACACATCCACATGGGC 1272
QY 4344 tgcacatggtacagatgacatttcacatgacacatataccacacatcttgcacgacaaa 4403
DB 1273 TGCACGCGCTTCGTCATCTTTGAGTGCACATGTGGCGCTACACAGCCACGACCGG 1332
QY 4404 tatgacttcacacacatataccacagagggcctgca 4438
DB 1333 TACGAGTCTCGTCGCACATTAACGGAGGGAGCA 1367

RESULT 14
US-08-283-300A-2
? Sequence 2, Application US/08283300A
? Patent No. 6172278
? GENERAL INFORMATION:
? APPLICANT: Georgopoulos, Katia A.
? TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
? NUMBER OF SEQUENCES: 26
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 STATE STREET, Suite 510
? CITY: BOSTON
? STATE: MASSACHUSETTS
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII (text)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/283,300A
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/238,212
? FILING DATE: 02-MAY-94
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/121,438
? FILING DATE: 14-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/946,233
? FILING DATE: 14-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Myers, Paul L.
? REGISTRATION NUMBER: 35,695
? REFERENCE/DOCKET NUMBER: MCP-027
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs

? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1386
? US-08-283-300A-2

Query Match 0.6%; Score 57.4; DB 4; Length 1386;
Best Local Similarity 60.6%; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtcactgtgacatgtcttcttgatgaagatgatagtatgttcataatagt 4343
DB 1213 AAGTGGCAACACTGCCGGGTGCTCTTCCTGGATCAGTCATGTACACATCCACATGGGC 1272
QY 4344 tgcacatggtacagatgacatttcacatgacacatataccacacatcttgcacgacaaa 4403
DB 1273 TGCACGCGCTTCGTCATCTTTGAGTGCACATGTGGCGCTACACAGCCACGACCGG 1332
QY 4404 tatgacttcacacacatataccacagagggcctgca 4438
DB 1333 TACGAGTCTCGTCGCACATTAACGGAGGGAGCA 1367

RESULT 15
US-08-711-417C-3
? Sequence 3, Application US/08711417C
? Patent No. 6228611
? GENERAL INFORMATION:
? APPLICANT: Georgopoulos, Katia A.
? TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
? NUMBER OF SEQUENCES: 202
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Fish & Richardson P.C.
? STREET: 225 Franklin street
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02110-2804
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: FASTSEQ for Windows Version 2.0b
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/711,417C
? FILING DATE: 05-Sep-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/238,212
? FILING DATE: 02-MAY-1994
? APPLICATION NUMBER: 08/121,438
? FILING DATE: 14-SEP-1993
? APPLICATION NUMBER: 07/946,233
? FILING DATE: 14-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Myers, Louis P.
? REGISTRATION NUMBER: 35,965
? REFERENCE/DOCKET NUMBER: 10287/007001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617/542-5070
? TELEFAX: 617/542-8906
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:

NAME/REV: Coding Sequence
LOCATION: 1...1383
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-711-417C-3

Query Match 0.68; Score 57.4; DB 4; Length 1386;
Best Local Similarity 60.6%; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtgactgtggcattgtcttccttgatgaagatgtatgtcttgcatatgagt 4343
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DB 1333 TACGAGTTCTCTCGCACATACGCGGAGGAGACA 1367

Search completed: July 21, 2002, 21:27:49
Job time: 22556 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 14:53:23 ; Search time 6987.25 Seconds

(Without alignments)
19925.019 Million cell updates/sec

Title: US-09-702-216-1
Sequence: 10315
1 ttctccgcgaagctcctt.....gttatttcaaaaaaaaaa 10315

Scoring table:

IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
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8: em_hic:*
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13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	837.2	8.1	842	9	AL535097
3	722	7.0	810	10	BI825385
4	713.4	6.9	824	10	BG254038
5	703.4	6.8	792	10	BI664283
6	693.2	6.7	765	10	BI596760
7	690	6.7	783	9	AV687506
8	681.6	6.6	691	9	AV687506
9	656.6	6.4	742	9	AV687506
10	652.8	6.3	886	10	AV687506
11	649.2	6.3	1043	10	BI686434
12	649	6.3	649	10	BI686434
13	648.6	6.3	813	9	BI686434
14	630	6.1	649	9	BI686434
15	629.4	6.1	679	10	BI686434
16	607.8	5.9	740	12	AG186896
17	606.8	5.9	650	9	BB641330

C 18	599.2	5.8	728	10	BI106944
19	594.8	5.8	598	9	AW303579
20	592.2	5.7	964	10	BI115118
21	592.2	5.6	917	10	BI178176
22	576.2	5.6	953	10	BI138096
23	571.8	5.5	602	12	AG025673
24	569	5.5	569	9	AW021592
25	567.8	5.5	749	10	BI139707
26	547	5.3	547	9	BI139707
27	546.4	5.3	584	9	BI139707
28	544.4	5.3	661	10	BI152146
29	541.6	5.3	569	9	AW021592
30	541.4	5.2	543	9	AW021592
31	539.8	5.2	567	10	BI1082772
32	539.8	5.2	925	10	BI1082772
33	536.8	5.2	925	10	BI1082772
34	531	5.1	729	10	BI168531
35	529.4	5.1	732	10	BI168531
36	529	5.1	542	9	BI168531
37	525.2	5.1	673	9	BI168531
38	525	5.1	525	10	BI168531
39	520.8	5.0	560	9	BI168531
40	520.2	5.0	566	9	BI168531
41	517	5.0	528	9	BI168531
42	513.6	5.0	521	9	BI168531
43	505.6	4.9	847	10	BI139728
44	503	4.9	503	9	AW070915
45	502	4.9	667	10	BI174562

ALIGNMENTS

RESULT 1	AL565773	928 bp	MRNA	linear	EST 16-FEB-2001
LOCUS	AL565773/c				
DEFINITION	AL565773 LTR-FL013-FBm1 Homo sapiens cDNA clone CS0DF008Y101 3				
ACCESSION	AL565773				
VERSION	AL565773.1				
KEYWORDS	GI:12917482				
SOURCE	human				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	Li, W.B., Gruber, C., Jesse, J., and Polyes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
CONTACT	Contact: Genoscope				
Genoscope	Genoscope - Centre National de Sequencage				
BP 191 91006 EVRY cedex - France					
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					

FEATURES

Location/Qualifiers

1..928

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DF008Y101"

/clone_lib="LTR-FL013-FBm1"

/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"

/lab_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT

319 a 164 c 148 g 280 t 17 others

ORIGIN

Query Match 8.5%; Score 879.8; DB 9; Length 928;
 Best Local Similarity 96.4%; Pred. No. 1e-123;
 Matches 895; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 7634 gaatttctcttggaaagcctcccttgatgaatgagtgccagtaaatg 7693
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 QY 7694 lgtgcattttaaactgaaatattttaaattatgtctatatttcaattagctt 7753
 DB 867 TGTGCATTATAAATGAAAAATTTTAAATTAATTTGCTATATTTCAATTAATGAGCTT 808
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 DB 747 TCTCTCATCTCTCATCT 688
 QY 7874 caaccacatcagaacgttgatgagagagacacacacacacacacacacacacacacac 7933
 DB 687 CAACCACTCAGACGTTGTGATGAGAGACACTACATACCTCCAGATATAGAGA 628
 QY 7934 aaaggacagagctcctcactgataactcgtatgctcaaaaggaaagagatgcccaatc 7993
 DB 627 AAAGACAGACCTCTAATGATTAACCTGTAGTCAAAAGAGAAAAGATGCCAATTC 568
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 QY 8054 taacatgctctttagtgaagtagatcttcttcttcttcttcttcttcttcttcttctt 8113
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 DB 208 GCTKCAAAACATSAACAAGTACCGGCTCTTGACACATGTAAGTCTGCTGCTGTTTAA 149
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 QY 8534 aggtcaactttagctactgcttcttggctt 8561
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RESULT 2

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 DEFINITION AL535097 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DP008y101 5
 prime, mRNA sequence.
 ACCESSION AL535097
 VERSION AL535097.1 GI:12798590
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE Li W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /clone_1lb="LTI_FL013_FBrn1"
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 week, 24 week and 26 week)"
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a Molt-Oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by life
 technologies. Contact : Peng Liang life technologies, a
 division of invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 filiang@life-tech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 249 a 130 c 126 g 337 t
 ORIGIN

Query Match 8.1%; Score 837.2; DB 9; Length 842;
 Best Local Similarity 99.6%; Pred. No. 3e-117;
 Matches 839; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 QY 7150 tagtgctggacaagaataggtcttatttttgagcatgacatttattcatt 7209
 DB 61 TAGGTGTGGACACAAATAGCTTCTTATTTTGGCATGATAGCTTTTATTTTCAAT 120
 QY 7210 caattttttttttctgagacagacatagatgacacacacacacacacacacacacacac 7269
 DB 121 CAATTTTTTTTTTTCTCAGACACACATAGTAGACATGCAATGCAATTAAT 180
 QY 7270 cactattcttgaaattatgctcagctcactttcttcttcttcttcttcttcttcttctt 7329
 DB 181 CACTATCTTGGAAATTTATGAGTACTCTTTTATTAATAAATTTTGGATGAGCGT 240
 QY 7330 tgaacagatagatctattcactccttcttattctgataatttatttcttcttctt 7389
 DB 241 TGACACATAGATCTTATTCATCTCTTTATTTATTTATTTATTTATTTATTTATTTT 300
 QY 7390 ctctcatcttatacatatttggltggaagaaggttggccttttttgaagaagacaaa 7449
 DB 301 CTTTCATTTATTTATTTTGGTGGAGAGAGTGGCTTTTGGCAAGACAAAA 360
 QY 7450 attattataacactaacactccttcttggacatttaagccttattcactccta 7509
 DB 361 ATTATTATAACACTAAACACTCTTTTGTGACATTTAAAGCTTTATTCATCTCTCA 420

LOCUS BC254038 824 bp mRNA linear EST 13-FEB-2001
 DEFINITION 60326675F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4475131 5',
 mRNA sequence.
 ACCESSION BG254038
 VERSION BG254038.1 GI:12763844
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 824)
 AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: DCMU/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.jnl.gov
 Plate: LLM10300 row: e column: 20
 High quality sequence stop: 699.
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 /db_xref="taxon:9606"
 /clone="IMAGE:4475131"
 /clone_1ib="NIH_MGC_91"
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site: 1: NCI;
 Site: 2: Salt; Cloned unidirectionally; oligo-dr primed.
 Average insert size 1.4 kb. Library enriched for
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 Note: this is a NIH-MGC library."
 BASE COUNT 265 a 205 c 180 g 174 t
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Query Match 5.9%; Score 713.4; DB 10; Length 824;
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 Matches 768; Conservative 0; Mismatches 36; Indels 3; Gaps 3;

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QY 3457 acggtgacagattatgaagagagaaacaaagccttaccagaagcacttcag 3516
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 Db 66 ACGGTGGACAGATTATTAGAGAGAGAAACAAAGGCGCTTAAACCAAGAGCATTGAG 125

QY 3517 ctgagagctcaacaaacagcagagggcgacgaatgagagcgaatcaatggaagccgt 3576
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 Db 126 CTGAGCAGCTCAACACACAGAGAGGCGACGATGAGAGCAGCATGATGAGAGCCCGT 185

QY 3577 taagagagagtcgaagatcatctaaactaaagctaccagaagaaatttccatccca 3636
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 Db 186 TAGAGAGAGAGTCAGAGATCATCTAACTAAAGTCAACACAGAGAAATTCACATCCCA 245

QY 3637 gccctaagtaatacgaagcccaagggttcattgactaaagacatcttgcacatccag 3696
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 Db 246 GCGTAAGTAAATACGAGAGCCGAGGTTGATGATTAAGGCATTCGCTGAGAGCAG 305

QY 3697 tctgttgagccaactctgatatctacaaagagtgacactttgcacatccagataa 3756
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 Db 306 TCCCTGGTCAGCAAACTCTGGATATTCACAAAGGATGCAACCTTGCACATTCAGATA 365

QY 3757 aaagtcctcaaggaagctgagatccagaagaaatagctatccgttcggaaggaag 3816
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 Db 366 AAAGTCCCTCAGGAAGTACTGAGATCCAGAGAAATGTTCAATCCGTATCGAAGGGAAG 425

QY 3817 gaagtcctgaagagagcagctctactagaaagtaacatgagacctgcgaaacaccacaa 3876
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QY 3937 tacataatccttccagagatgagcctgattgctcggcttgcagtaataaataac 3996
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 Db 725 CAATGAATTCCTCTGATGATTGGGATCAAGCATACCAAGACTGGG-CAACTCAAAAGCT 783

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RESULT 5
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 VERSION B1664283.1 GI:15578516
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 SOURCE house mouse.
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 Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 792)
 AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.jnl.gov
 Plate: LLM1819 row: j column: 10
 High quality sequence stop: 791.
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 /dev_stage="5 months"
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 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: Salt;
 Site: 2: NCI; Cloned unidirectionally. Primer: Oligo dr.
 library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 237 a 191 c 172 g 192 t

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Shimizu, S., Saito, K., Kawai, Y.,
Y., Nagai, T., Sugano, S. and

one pass sequencing. Helix

Construction: Department of
ce, University of Tokyo, and

mainly need
5 others

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DB 9; length 742;
-90;
8; indels 5; Gaps 5;
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530-539aa 535-544aa 550-559aa 565-574aa 580-589aa 595-604aa 610-619aa 625-634aa 640-649aa 655-664aa 670-679aa 685-694aa 700-709aa 715-724aa 730-739aa 745-754aa 760-769aa 775-784aa 790-799aa 805-814aa 820-829aa 835-844aa 850-859aa 865-874aa 880-889aa 895-904aa 910-919aa 925-934aa 940-949aa 955-964aa 970-979aa 985-994aa 1000-1009aa 1015-1024aa 1030-1039aa 1045-1054aa 1060-1069aa 1075-1084aa 1090-1099aa 1105-1114aa 1120-1129aa 1135-1144aa 1150-1159aa 1165-1174aa 1180-1189aa 1195-1204aa 1210-1219aa 1225-1234aa 1240-1249aa 1255-1264aa 1270-1279aa 1285-1294aa 1300-1309aa 1315-1324aa 1330-1339aa 1345-1354aa 1360-1369aa 1375-1384aa 1390-1399aa 1405-1414aa 1420-1429aa 1435-1444aa 1450-1459aa 1465-1474aa 1480-1489aa 1495-1504aa 1510-1519aa 1525-1534aa 1540-1549aa 1555-1564aa 1570-1579aa 1585-1594aa 1600-1609aa 1615-1624aa 1630-1639aa 1645-1654aa 1660-1669aa 1675-1684aa 1690-1699aa 1705-1714aa 1720-1729aa 1735-1744aa 1750-1759aa 1765-1774aa 1780-1789aa 1795-1804aa 1810-1819aa 1825-1834aa 1840-1849aa 1855-1864aa 1870-1879aa 1885-1894aa 1900-1909aa 1915-1924aa 1930-1939aa 1945-1954aa 1960-1969aa 1975-1984aa 1990-1999aa 2005-2014aa 2020-2029aa 2035-2044aa 2050-2059aa 2065-2074aa 2080-2089aa 2095-2104aa 2110-2119aa 2125-2134aa 2140-2149aa 2155-2164aa 2170-2179aa 2185-2194aa 2200-2209aa 2215-2224aa 2230-2239aa 2245-2254aa 2260-2269aa 2275-2284aa 2290-2299aa 2305-2314aa 2320-2329aa 2335-2344aa 2350-2359aa 2365-2374aa 2380-2389aa 2395-2404aa 2410-2419aa 2425-2434aa 2440-2449aa 2455-2464aa 2470-2479aa 2485-2494aa 2500-2509aa 2515-2524aa 2530-2539aa 2545-2554aa 2560-2569aa 2575-2584aa 2590-2599aa 2605-2614aa 2620-2629aa 2635-2644aa 2650-2659aa 2665-2674aa 2680-2689aa 2695-2704aa 2710-2719aa 2725-2734aa 2740-2749aa 2755-2764aa 2770-2779aa 2785-2794aa 2800-2809aa 2815-2824aa 2830-2839aa 2845-2854aa 2860-2869aa 2875-2884aa 2890-2899aa 2905-2914aa 2920-2929aa 2935-2944aa 2950-2959aa 2965-2974aa 2980-2989aa 2995-3004aa 3010-3019aa 3025-3034aa 3040-3049aa 3055-3064aa 3070-3079aa 3085-3094aa 3100-3109aa 3115-3124aa 3130-3139aa 3145-3154aa 3160-3169aa 3175-3184aa 3190-3199aa 3205-3214aa 3220-3229aa 3235-3244aa 3250-3259aa 3265-3274aa 3280-3289aa 3295-3304aa 3310-3319aa 3325-3334aa 3340-3349aa 3355-3364aa 3370-3379aa 3385-3394aa 3400-3409aa 3415-3424aa 3430-3439aa 3445-3454aa 3460-3469aa 3475-3484aa 3490-3499aa 3505-3514aa 3520-3529aa 3535-3544aa 3550-3559aa 3565-3574aa 3580-3589aa 3595-3604aa 3610-3619aa 3625-3634aa 3640-3649aa 3655-3664aa 3670-3679aa 3685-3694aa 3700-3709aa 3715-3724aa 3730-3739aa 3745-3754aa 3760-3769aa 3775-3784aa 3790-3799aa 3805-3814aa 3820-3829aa 3835-3844aa 3850-3859aa 3865-3874aa 3880-3889aa 3895-3904aa 3910-3919aa 3925-3934aa 3940-3949aa 3955-3964aa 3970-3979aa 3985-3994aa 4000-4009aa 4015-4024aa 4030-4039aa 4045-4054aa 4060-4069aa 4075-4084aa 4090-4099aa 4105-4114aa 4120-4129aa 4135-4144aa 4150-4159aa 4165-4174aa 4180-4189aa 4195-4204aa 4210-4219aa 4225-4234aa 4240-4249aa 4255-4264aa 4270-4279aa 4285-4294aa 4300-4309aa 4315-4324aa 4330-4339aa 4345-4354aa 4360-4369aa 4375-4384aa 4390-4399aa 4405-4414aa 4420-4429aa 4435-4444aa 4450-4459aa 4465-4474aa 4480-4489aa 4495-4504aa 4510-4519aa 4525-4534aa 4540-4549aa 4555-4564aa 4570-4579aa 4585-4594aa 4600-4609aa 4615-4624aa 4630-4639aa 4645-4654aa 4660-4669aa 4675-4684aa 4690-4699aa 4705-4714aa 4720-4729aa 4735-4744aa 4750-4759aa 4765-4774aa 4780-4789aa 4795-4804aa 4810-4819aa 4825-4834aa 4840-4849aa 4855-4864aa 4870-4879aa 4885-4894aa 4900-4909aa 4915-4924aa 4930-4939aa 4945-4954aa 4960-4969aa 4975-4984aa 4990-4999aa 5005-5014aa 5020-5029aa 5035-5044aa 5050-5059aa 5065-5074aa 5080-5089aa 5095-5104aa 5110-5119aa 5125-5134aa 5140-5149aa 5155-5164aa 5170-5179aa 5185-5194aa 5200-5209aa 5215-5224aa 5230-5239aa 5245-5254aa 5260-5269aa 5275-5284aa 5290-5299aa 5305-5314aa 5320-5329aa 5335-5344aa 5350-5359aa 5365-5374aa 5380-5389aa 5395-5404aa 5410-5419aa 5425-5434aa 5440-5449aa 5455-5464aa 5470-5479aa 5485-5494aa 5500-5509aa 5515-5524aa 5530-5539aa 5545-5554aa 5560-5569aa 5575-5584aa 5590-5599aa 5605-5614aa 5620-5629aa 5635-5644aa 5650-5659aa 5665-5674aa 5680-5689aa 5695-5704aa 5710-5719aa 5725-5734aa 5740-5749aa 5755-5764aa 5770-5779aa 5785-5794aa 5800-5809aa 5815-5824aa 5830-5839aa 5845-5854aa 5860-5869aa 5875-5884aa 5890-5899aa 5905-5914aa 5920-5929aa 5935-5944aa 5950-5959aa 5965-5974aa 5980-5989aa 5995-6004aa 6010-6019aa 6025-6034aa 6040-6049aa 6055-6064aa 6070-6079aa 6085-6094aa 6100-6109aa 6115-6124aa 6130-6139aa 6145-6154aa 6160-6169aa 6175-6184aa

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 Db 361 ACATTCAATATAAAGTCTCCAGGAAAGTACTGAGATCCAGAAATAGTTATCTCGTAT 420
 QY 3805 ctgaagggaagaagtgctcag 3864
 Db 421 CTGAAGGGAAGAGAGTCTGAG 480
 QY 3865 aac 3924
 Db 481 AACACCCAAATTTATTCACACACAGGACCCCTATTGAAAGTACCAAGTACCCAGCTTTTG 540
 QY 3925 gactlcccttgatcag 3983
 Db 541 GNCCTTCCCTTTGT-CATATGACTTCCAGAGTGAAGTATTTGGCTGGGGTCTGGAGGT 599
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 Db 600 AAATATAAGCTCTCCGTTCTCGGGAATCCGCACTACTTGAGTCAAGTGGCTGGCTAAC 659
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RESULT 10
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 LOCUS 603312804F1 NCI_GCAP_Mam6 Mus musculus CDNA IMAGE:5552984 5',
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 VERSION B1686434.1 GI:15649062
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.

REFERENCE
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.C.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM11897 row: 9 column: 01
 High quality sequence stop: 772.
 Location/Qualifiers
 1. 886

FEATURES

FEATURES
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BASE COUNT 268 a 248 c 189 g 181 t
 ORIGIN
 Query Match 6.3%; Score 652.8; DB 10; Length 886;
 Best Local Similarity 90.1%; Pred. No. 2.5e-89;
 Matches 744; Conservative 0; Mismatches 77; Indels 5; Gaps 4;

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 QY 3430 ggccttcaacatcaataaacaac 3489
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 Db 205 AGCGCTTAACCCAGAGGACCTTCAAGGCTGAGCAGCTCAACAAACGAGAGAGAGAGAG 264
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 Db 505 AATAGTTCAATCCGATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 564
 QY 3848 gtacatgagagac 3907
 Db 565 GTACATGAGACCTGCAAAACCCCAACTATTTCCACAGGAGAGAGAGAGAGAGAGAGAGAG 624
 QY 3908 ccagtcac 3967
 Db 625 CCATACCCCGCTTTGGAGTACCTTATGATACATTAATGATTCAGAGTGAAGCTGATG 684
 QY 3968 gctgagcttctgag 4026
 Db 685 GCTACGCTTCTGAGAGAAATATTAAGCTCTCGCTTCTGGAATTCGCACTCTGCACTC 744
 QY 4027 acgctgctgagac 4086
 Db 745 ATGTCCTGCTTACCAAAATCTTCCCAAAACCTATGTCCTTATTCACCTACCACTG 804
 QY 4087 ctctcacttttctgctg-cttgatcagacacacacacacacacacacacacacacacacacacac 4130
 Db 805 CTCCTCATTTCCAGACGACGACGATCAGACATTCACATCCCTCA 850

RESULT 11
 B9982937 1043 bp mRNA linear EST 23-JAN-2001
 LOCUS B9982937
 DEFINITION 602306330F1 NIH_MGC_88 Homo sapiens CDNA clone IMAGE:4397719 5',
 ACCESSION B9982937
 VERSION B9982937.1 GI:12385749
 KEYWORDS EST.

SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1043)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Invitrogen Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10098 row: 1 column: 08
High quality sequence stop: 642.
Location/Qualifiers
1..1043
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4397719"
/clone_lib="NIH-MGC-88"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
Oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC library."
BASE COUNT 317 a 260 c 293 g 173 t
ORIGIN

Query Match 6.3%; Score 649.2; DB 10; Length 1043;
Best Local Similarity 95.1%; Pred. No. 8.3e-89;
Matches 702; Conservative 0; Mismatches 33; Indels 3; Gaps 3;

3022 gaggggagagacatctctgaggggagtcctgcataccccaagaagcctggggtgta 3081
11 GAGGGGAGACATCTCTGCGGGGAGTCCGTCATACACCACCAAGCCTGGGCTGCTGA 70
3082 cgcctgtctgcacccaagagagagac-aaagacttaagagatgcccaatggagag 3140
71 CGCCTGTCTGCGACCCCAAGAGAGAGCAAGAACTCTAAGGAGATGCCAATGTGAG 130
3141 gccgccatctggcgagacactattatgcttggctgtgagaaacaaagagattcctg 3200
131 GCGAGCATCTGCGCGCGAGCATTTATGCTTGGCTGGAACCAAGCGATTCCTGAG 190
3201 gggggcgagcgtggcgagaaatctcgggggcccctcccgagcagttatcgtgagga 3260
191 GGGGCGCAGCTGGCGAGAGAAAGTGTGGGCCCTCCCGCAGCAAGTATCTGATGGGA 250
3261 gaaacaagctcccaagatgaatcccaagctccctgtttagagagcgctcagctgtt 3320
251 GAAACAAGTCCCAAGATGAATCCCAAGCTCCTGTACGAGAGCCCTGAAGCTCGT 310
3321 ttltgtgcaattgctgcagcaacaagaacctctctctggcgaaagaatgcaatggcga 3380
311 TTTTGTGCCAATTGCTGACCAAGACCTCTCTCTGCGCAAGAAATGCAAAATGGCGGA 370
3381 tatgtatgaagcgtgtgacctctacagaagcttaactgactcccaagccttaaac 3440
371 TATGTATGCAAGCGTGTGGCTCTTACCAAGCTTCACTGACTCCCAAGGCTTTAAAC 430
3441 atcaataaacaacaacagctgtgagcagattatagagagagaaacaagaagcgctaac 3500
431 ATCAATAAACAACAACAGCGTGAAGCAATTTATTAAGAGAGAGAAAGAAAGCCCTTAAC 490
3501 cgaagagcacttcagagctcgaagcagctcaacaacaagcagagggcgaatgaagagca 3560

Db 491 CCAGAGGACTTCAAGCTGAGCAGCTCAACAAAGCAGAGGGCAGCATAGAGAGCAA 550
Qy 3561 gtaactgaagcccgcttagagagagagcagaagaatcatctactgaagtcacagaga 3620
Db 551 GTCMAATGAAGCCCGTTAGAGAGAGGCTCAAGAAATCATCTAAGTACCAAGAGA 610
Qy 3621 gaattcactcccccagccttaaglaatacgaagcccaaggtt-cattgaactaagaacca 3679
Db 611 GAATTCGA-TCCCGACAGTAAGTAATATGCAAGCCAGCGCTTCATTGAGTAAAGGCA 669
Qy 3680 ttctgtcagagcagcagctcctgttagcccaacitctgataltcacaagaagagcaac 3739
Db 670 TTCTGTGTCAGAGCAGCTCTGCTTCAGCAAAACTGTGGATTTCACAAAGTTGCAACC 729
Qy 3740 ttgacatcagaataa 3757
Db 730 TTGGCCCTTATATACAA 747

RESULT 12
LOCUS B1492548/c 649 bp mRNA linear EST 28-AUG-2001
DEFINITION B1492548
IMAGE:2484612 3', mRNA sequence.
ACCESSION B1492548
VERSION B1492548.1 GI:15331892
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
95130111
Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
B-1gham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
<http://www.nisc.nih.gov>).
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLM6182 row: K column: 13
Seq primer: 5' primer:
Location/Qualifiers
1..649
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2484612"
/clone_lib="Morton Fetal Cochlea"
/issue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ear; Vector: Bluescript SK-; Site_1: EcoRI;
Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dr. fetal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-TAP
XR Vector. Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATTCGCGCAGAG 3' -3' adaptor
sequence: 5' CTCGACTTTTCTTTTCTTTT 3'."
BASE COUNT 217 a 131 c 97 g 204 t
ORIGIN

Query Match 6.3%; Score 649; DB 10; Length 649;
 Best Local Similarity 100.0%; Pred. No. 1e-88;
 Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7918 ctccaagatatagtgaagaagacagagctcaattgtaactctgtagtctcaagaagaa 7917
 DB 649 CTCCAAGATATGACAAAGACAGACCTCTAATTGATACCTGTGATTCACAAAGAAA 590
 QY 7978 aagatagcccacattctctacatagacalattagatttttttaatacaatttaaga 8037
 DB 589 AGAGATATCCCAATTCCTACATGACATATTGAGATTTTATTAATCACTTTTAAAGA 530
 QY 8038 tagtgatgtctcttcttaaacctgtctgttttagtgaaaggtagattttataaacaagc 8097
 DB 529 TAGTATGTCTCTGTCTTAACGTCTCTTTTACTGAGTAGATTTTATTAACAAAGC 470
 QY 8098 atggagattctttctcaagtaataataagaaggaagaaagatcttaacagctc 8157
 DB 469 ATGGGANTCTTTTCTAAGCTAATATTAAAGAGGAAAAAGATCTTTAACAGCTC 410
 QY 8138 ttltglaagccctgltgagacattatqtlataattgacatgacataatctatt 8217
 DB 409 TTTCTGAAGCCTGTGTGACATATTATGTTAATTCACATGTCACATTAATTAAT 350
 QY 8218 atgataatgcaaatagagctcccaaaatattaaatgtatataatttaaatgctg 8277
 DB 349 ATGATCCAAATGCAATACAGCTCCCAAAATTAATTAATTAATTAATTAATTAAT 290
 QY 8278 aggaatacatctttcttaataaactgaagagctcgaatgagcttaataataattatt 8337
 DB 289 AGGAATACATTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 230
 QY 8338 agccctcgtltgltgagcagcaaaacalcaacaagtgacagctcttgagacttgagac 8397
 DB 229 AGCCTCTGTGTGTGCGTCGCAAAAACATCAAGAGACCGCTCTTGAGACCTGTGAAC 170
 QY 8398 gctgcccgtttagtaataataataatgattctcagagggggaatactctgcacatcag 8457
 DB 169 GCTGCCCTGTTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 110
 QY 8458 tggtagaaatgtagaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8517
 DB 109 TCGTGCAAAATGCGATGAAGAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 50
 QY 8518 gcccttaagttgagaggaagctcaacttaagtaactgtcttggcttgaga 8566
 DB 49 GCCTTAAGTTGAGAGGAGTCACTTACTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 13

LOCUS AU117784 813 bp mRNA linear EST 19-OCT-2000
 DEFINITION AU117784 HEMBA1 Homo sapiens cDNA clone HEMBA1002177 5', mRNA
 ACCESSION AU117784
 VERSION AU117784.1 GI:10932779
 KEYWORDS EST.
 SOURCE Human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 813)
 AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saiko,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951

Fax: 81-438-52-3952
 Email: genomeseht.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source location/Qualifiers
 1..813
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1002177"
 /clone_lib="HEMBA1"

/tissue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: pME18SFL3"
 BASE COUNT 250 a 193 c 183 g 184 t 3 others
 ORIGIN

Query Match 6.3%; Score 648.6; DB 9; Length 813;
 Best Local Similarity 96.3%; Pred. No. 1.e-88;
 Matches 685; Conservative 0; Mismatches 21; Indels 5; Gaps 2;

QY 2107 cagaagagagacaaatgaccacagacagacagagctcagtgaggctaaagaagagact 2166
 DB 97 CAGAAAGAGACAAATGACCAAGACAGACAAAGACCTGAGCTGAGCTGAGCTGAGCT 156
 QY 2167 tctcagaagaaggagccaggaataatgtaacagactaaattgtcagttcgtgact 2226
 DB 157 TCTCCAGCAAGGAGCCGACGATTAATAGTAAAGACCTTAATTTGCTGCTGTGACT 216
 QY 2227 tccgatatccaaagacatgagccctgagtgaattgagtgagtgagcactctccgactt 2286
 DB 217 TCCGATTTCCAAACCAATGACCTGCTGATTAATTAATTAATTAATTAATTAATTAAT 276
 QY 2287 atcaagagctcgaataatcaatcaagtgatcaatcaatcaatcaatcaatcaatcaat 2346
 DB 277 ATCAACAGCTCCATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 336
 QY 2347 gacttgcagcccaagaagacaccttggagaattactatccgttttctgttgagaataa 2406
 DB 337 GACTTTGCACCCGAGAAAGCACTTGGAGAAATTAATTAATTAATTAATTAATTAATTAAT 396
 QY 2407 gtaattgtcccaactgtgactctgtctgtcactgtctcctctgagcgctggaagct 2466
 DB 397 GTAATTTGTTCCACTGCTGACTTGTCTGTGACTTGTCTGTGACTTGTCTGTGACTTGT 456
 QY 2467 cgcagagcaaatcaatgagcagatgagtgatcattcaacacccctgaagtatgactcc 2526
 DB 457 CGCAGTCAAAATCAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
 QY 2527 tcttcaactatgaagtgatgagtgatgagtgatgagtgatgagtgatgagtgatgagtg 2586
 DB 517 TCTTTCACTATGATAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
 QY 2587 acctgcaagatcagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2646
 DB 577 ACCTGCAAGATCGATGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 636
 QY 2647 aatgtatt 2706
 DB 637 AATGTATTTTATTATCCCAAGTGGAAAGAAAGATTTCCTCCGACACTACAGAGACACAA 696
 QY 2707 gctgtacaaatgagcgtcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2764
 DB 697 GCTGCTAAATGCGCTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 756
 QY 2765 ggaacttaaacactgtt---caatgcaagaacagacatcaactacagcaaa 2812
 DB 757 GCACCTTAACACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807

RESULT 14

AU117175 649 bp mRNA linear EST 19-OCT-2000
 LOCUS AU117175 HEMBA1 Homo sapiens cDNA clone HEMBA1000822 5', mRNA
 DEFINITION sequence.
 ACCESSION AU117175
 VERSION AU117175.1 GI:10932121
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
 FEATURES
 location/Qualifiers
 source 1..649
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1000822"
 /clone_lib="HEMBA1"
 /tissue_type="whole embryo, mainly head"
 /dev-stage="embryo, 10 weeks"
 /note="Vector: pME18SFl3"

BASE COUNT 207 a 109 c 121 g 209 t 3 others
 ORIGIN
 Query Match 6.1%; Score 630; DB 9; Length 649;
 Best Local Similarity 99.5%; Pred. No. 7.9e-86;
 Matches 641; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5306 gatgaaccagatgattgcttcttaagcctcctgtgtgttaactaactcactgcca 5365
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 Db 1 GATGAACCAAGTATGAGATTCTTTCTTAAGCTCTCTGTGGTTACTTAATCTCACTTGGCA 60
 QY 5366 catataactaaaggaatcccccattcaaaagcatagattgatacaaatgtcagaccy 5425
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CATATTAACITAAAGGATCCCTCAATTCMAAGCATAGATGATCAATATCTCAGACCG 120
 QY 5426 tgggttaattgttagaacaagcattctcttaacaaggaacccgtctattatt 5485
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 TGGCTTAATTTGTTTGAACACATGGCATTTCTTCAACAGGTAACCTCTCTATTTATTT 180
 QY 5486 tatlctclttggtlaataataatlcocaaactlgtgcagagcagctcaagtttac 5545
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 Db 181 TATTTCTTTGGTTAAATATATTTCCAACTTTGGTCAGGCGAGCTTAAAGTTTAC 240
 QY 5546 gttaacaaagactgcaagttgtatatagtaccagcaatccctcaataatgatacag 5605
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 Db 241 GTTACCAACAGCTGACAGTGGTATATGTACACCAATCCCTTCAATTAATGATACAG 300
 QY 5606 attagtaagtagcattaaataggaattcctagaagaatgtctctatagaactttaata 5665
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AATTATGTTAACTACATTAATAGGATCTTTAGAAAGTATGCTCTCAATCAACTTTTAAATA 360
 QY 5666 cttaagacttgcataaaactatccatgaaggaagctcctcagcactaacgcctcagga 5725
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CTTAAGCTTTGTTAAAACTATTCATCATGAAGGAAAGCTCTCTCAGCATTAATCTCTCAGGCA 420

QY 5726 aataggctaaataactgaacataataatattggttaagggcgtgttagctgagcctca 5785
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 Db 421 AATAGGGCTAAATAACTGAACATTAATTAATTTGTTAAAGGTGCTGTAGTCAAGCTCA 480
 QY 5786 atgcttgcacaagatgtaagcaggaacttaacttaattgattatattgltcc 5845
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 Db 481 ATGCTTCCTACAGCATGTATGTACAAAGCATCTATTATTAATTTGGCATTAATTTGTC 540
 QY 5846 caaccagtagtattatttttgcacagagatgtagaagatlatcaagaactactgagca 5905
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 Db 541 CAACAGTAAGTTATTTTGGCAGGAGATGTANAGATTAATTAACACTCTGTGATGCA 600
 QY 5906 ct-gtcagtaactatttcaatgaagaagttgggaagacaa 5948
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 CTGCTGAGTTAATTAATTTCAATTAAGAGTTGGAGAGCAAA 644

RESULT 15
 LOCUS BG779571 679 bp mRNA linear EST 15-MAY-2001
 DEFINITION BG779571 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:480793 5', mRNA sequence.
 ACCESSION BG779571
 VERSION BG779571.1 GI:14049888
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 679)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9qab3-rt@mail.nih.gov
 Tissue procurement: DCTP/DRP
 cDNA library preparation: CLONETECH Laboratories, Inc.
 cDNA library arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: <http://image.lnl.gov>
 Plate: L10M160 row: C column: 02
 High quality sequence stop: 679.
 FEATURES
 location/Qualifiers
 source 1..679
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:480793"
 /clone_lib="NIH_MGC_60"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggccctggcc); Site 2: Sfil (ggccattagggc 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCAGCATG-dT(30)-BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC library."

BASE COUNT 224 a 107 c 129 g 218 t 1 others
 ORIGIN
 Query Match 6.1%; Score 629.4; DB 10; Length 679;
 Best Local Similarity 99.1%; Pred. No. 9.6e-86;
 Matches 674; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
 QY 5505 ataattccaacttgtgtcagcagcgtcctaagttacgttaccacaagactgcaagt 5564

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Db      1  |||||||
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Qy      5565  |||||||
          TGGTATATGTCACGACCAATCCCTTCATTTAAATGTATACAGATTTAGTTAACTACATTA 120
Db      61  |||||||
          TGGTATATGTCACGACCAATCCCTTCATTTAAATGTATACAGATTTAGTTAACTACATTA 120
Qy      5625  |||||||
          AATAGGATTCCTTAAAGATATGTCCTCATAGAACTTTAAATCTTAAGSCTNTGTAAAC 180
Db      121  |||||||
          5685  TATCCATGAAAGCGGAAGCTCCCTCAGCATAACTGCTCAGGGAATVAGGCTAAATACCTGA 240
          181  TATCCATGAAAGCGGAAGCTCCCTCAGCATAACTGCTCAGGGAATVAGGCTAAATACCTGA 240
Qy      5745  |||||||
          AATATAATATGTTAAAGGTGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 300
Db      241  |||||||
          5805  ATGTACAAAGACTGACTTAAATTAATTTGCAATTAATTTGCAATTAATTTGCAATTAATTT 360
          301  ATGTACAAAGACTGACTTAAATTAATTTGCAATTAATTTGCAATTAATTTGCAATTAATTT 360
Qy      5865  |||||||
          361  TGCCACGAGATGTACAGATATTAACAGCTACTGATGATGATGATGATGATGATGATGAT 420
          5925  CATTAAAGAGTTGGAGACAAATAGCAAAAAAACCTTATTTTCTAGTAAATATT 480
          421  CATTAAAGAGTTGGAGACAAATAGCAAAAAAACCTTATTTTCTAGTAAATATT 480
Qy      5984  |||||||
          481  AATGTATTTACATTTCAAAATTAATGTCCTGACATTAATTAATTAATTAATTAATTAATTA 540
          6043  ACGTATGCAAAACATTTTCCATCATGCAATTAAGTCAATTTGCTGCTGCTGCTGCTGCTGCT 600
          541  ACGTATGCAAAACATTTTCCATCATGCAATTAAGTCAATTTGCTGCTGCTGCTGCTGCTGCT 600
Qy      6103  |||||||
          601  TTACATTTGTCGAAATGTAGCAAAACAGTAATGCAAGCAAACTTTTCTATGCACTAGATA 660
          6162  TCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
          661  TCC-TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 679

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Search completed: July 21, 2002, 18:02:27
 Job time: 11344 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 16:51:33 ; Search time 11495.2 Seconds

(without alignments)
19413.717 Million cell updates/sec

Title: US-09-702-216-1
10315
Perfect score: 1
Sequence: 1 ttcctccgcgaagctcctt.....gtttatltcaaaaaaaaaa 10315

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	10278.2	99.6	10320	19	US-09-525-361-32
3	10278.2	99.6	10320	19	US-09-525-361-32
4	10011	97.1	10011	69	US-60-306-501-103
5	9951	96.5	10006	1	PCT-US00-32056-20
6	9951	96.5	10006	29	US-09-721-183-20
7	6774.6	65.7	10246	1	PCT-US01-01334-6816
8	6774.6	65.7	10246	30	US-09-764-874-6816
9	6774.6	65.7	10246	37	US-10-092-400-6816
10	6587.2	63.9	10004	1	PCT-US01-01334-6814
11	6587.2	63.9	10004	30	US-09-764-874-6814
12	6587.2	63.9	10004	37	US-10-092-400-6814
13	5793	56.2	5825	1	PCT-US01-01334-6815
14	5793	56.2	5825	30	US-09-764-874-6815
15	5793	56.2	5825	37	US-10-092-400-6815
16	5136.8	49.8	5184	36	US-09-976-594-484
17	5136.8	49.8	5184	63	US-09-976-594-484
18	5136.8	49.8	5184	71	US-60-240-409-484
19	2654.6	22.0	2662	57	US-60-324-185-35824
20	2272	22.0	2328	53	US-60-244-468-1604
21	2269.6	22.0	2328	57	US-60-185-215-383
22	2269.6	22.0	2328	22	US-09-585-879-222
23	2257.6	21.9	2327	56	US-60-177-360-4452
24	2257.6	21.9	2327	1	PCT-US00-32056-3
25	2230.6	21.6	2677	29	US-09-721-183-3
26	1549.2	15.0	1578	66	US-60-360-207-12615
27	1545	15.0	1590	26	US-60-278-232-10896
28	1545	15.0	1590	66	US-09-668-179-203
29	1372.4	13.3	1743	75	US-60-156-625-3003
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			55	55	US-60-168-432-279

Sequence 190, App
Sequence 25248, A
Sequence 107, App
Sequence 107, App
Sequence 107, App
Sequence 107, App
Sequence 107, App
Sequence 107, App
Sequence 107, App
Sequence 134, App
Sequence 9624, Ap
Sequence 8751, Ap
Sequence 11, Appl
Sequence 2688, Ap
Sequence 8850, Ap

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ctctctc	300

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Db	7201	atttcaatcaatttttttttcttccagacagatagtagtalcacatgacattgga	7260
QY	7261	aattcatcatcactattcttggaaatttatatgtrcagttcacttttgaataatttt	7320
Db	7261	aattcatcatcactattcttggaaatttatatgtrcagttcacttttgaataatttt	7320
QY	7321	ggaatagcgttgcacagatagatcttcatcaacttccttattatgaataattttt	7380
Db	7321	ggaatagcgttgcacagatagatcttcatcaacttccttattatgaataattttt	7380
QY	7321	ggaatagcgttgcacagatagatcttcatcaacttccttattatgaataattttt	7380
Db	7321	ggaatagcgttgcacagatagatcttcatcaacttccttattatgaataattttt	7380
QY	7381	catttttgcttcatattatatacatatttggtygagaagagtttggccttttga	7440
Db	7381	catttttgcttcatattatatacatatttggtygagaagagtttggccttttga	7440
QY	7441	gagagcaaaatttatataaacaactacactcttcttggacatataaagccttatc	7500
Db	7441	gagagcaaaatttatataaacaactacactcttcttggacatataaagccttatc	7500
QY	7501	catctccacagaatatataaacttatatttttaatttaagaatctcgaattatcta	7560
Db	7501	catctccacagaatatataaacttatatttttaatttaagaatctcgaattatcta	7560
QY	7561	tcttaaatatgtaattttaacagagctattatgtaacoggaactttttaagaattt	7620
Db	7561	tcttaaatatgtaattttaacagagctattatgtaacoggaactttttaagaattt	7620
QY	7621	catgatactttaggaattctctcttggaagaagcttccctcttgatgaatgattg	7680
Db	7621	catgatactttaggaattctctcttggaagaagcttccctcttgatgaatgattg	7680
QY	7681	ccagatgaatattgtygcacatttaaaactcgtgaatattttaaatatttgcataat	7740
Db	7681	ccagatgaatattgtygcacatttaaaactcgtgaatattttaaatatttgcataat	7740
QY	7741	ctaataatgcttggatcaataaactttaggcagagacagatcgtcttcatactcc	7800
Db	7741	ctaataatgcttggatcaataaactttaggcagagacagatcgtcttcatactcc	7800
QY	7801	ttttcccatctttcttccatcacatcactcgtatataatcgtgttggatagaagaa	7860
Db	7801	ttttcccatctttcttccatcacatcactcgtatataatcgtgttggatagaagaa	7860
QY	7861	aatcataaagagcaaacacatctcgaagaagtttggattgagagagaacatcagatc	7920
Db	7861	aatcataaagagcaaacacatctcgaagaagtttggattgagagagaacatcagatc	7920

Dh	9001	caactgagaagaaatgtgaaatcagaagtataccacaacgtgtgaaacattcagacaatgttaca	9060
Qy	9061	ttcatgtgtctctcttggaaagggaagggagcgtglaagccttcaactcgtctctcaaccgga	9120
Dh	9061	ttcatgtgtctctcttggaaagggaagggagcgtglaagccttcaactcgtctctcaaccgga	9120
Qy	9121	gaaagcaggaataaacttaaccgtggaataatgtttcgcctttatcagaagaatgtgc	9180
Dh	9121	gaaagcaggaataaacttaaccgtggaataatgtttatagcttttatcagaagaatgtgc	9180
Qy	9181	ctttacagatagatagctcccaaacctcaatcctgttttcccccgttttttttttttttt	9240
Dh	9181	ctttacagatagatagctcccaaacctcaatcctgttttcccccgttttttttttttttt	9240
Qy	9241	ttttcccaacahatgaaactgacagatataccttttcttttggcttcgaagttcccca	9300
Dh	9241	ttttcccaacahatgaaactgacagatataccttttcttttggcttcgaagttcccca	9300
Qy	9301	ccgttaaatatgaaaaataatglatatlaataatattatlaataataatgtaatgta	9360
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Qy	9361	gtactgtttgtgaaagcacttggatgactcctgtgtgaaaggccacatgaggtgccagt	9420
Dh	9361	gtactgtttgtgaaagcacttggatgactcctgtgtgaaaggccacatgaggtgccagt	9420
Qy	9421	attattatgbyggccaagggggttalttlaaacgttgaattcccaaggccaaggaaggttg	9480
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Qy	9481	gggtgcattttctcttaagaacgagcgttaatatcatcaactcaggccaatagtgtgtacta	9540
Dh	9481	gggtgcattttctcttaagaacgagcgttaatatcatcaactcaggccaatagtgtgtacta	9540
Qy	9541	tgaagatgcaaaacattcactagcgtgataaataatagtttcttaatggtccaccaataa	9600
Dh	9541	tgaagatgcaaaacattcactagcgtgataaataatagtttcttaatggtccaccaataa	9600
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Dh	9601	ggccaatatccacaataaagcgaacaattctctttagggcgactatttgacacacactg	9660
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Qy	9721	tacagcaaatatccaacggcaggaagaatgctttccatagsgaataattctgtgtctaaga	9780
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Qy	9781	aaaaagaatcattttagtacctgaatttgaatbaabagaatggtgcataatagtctgtc	9840
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Qy	9961	atgtcgtatgaatcctaactctgataataaagttttaccccaagttacacataacggcgt	10020
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Qy	10021	tggtatggtttatattggtatcacttcatcctcttaggcaatatggyaaatacagatcaatt	10080
Dh	10021	tggtatggtttatattggtatcacttcatcctcttaggcaatatggyaaatacagatcaatt	10080
Qy	10081	gaaatataataataataataacaggtctgcgtgaatggaatggtgaaatcaatcac	10140

[illegible]

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Db	1261	tgaaagagacacccagaccccggaacctctgtctccagaagcttcagagacttaataatgacaata	1320
QY	1315	tcgttgagatatgttctactacgacagacacccacagactatataaagcacttcgcgaagt	1374
Db	1321	tcgttgagatatgttctactacgacagacacccacagactatataaagcacttcgcgaagt	1380
QY	1375	atcaacttaggaactgtacaacgcgacagcgaagatgtgagctgtgagacagaaatcttgg	1434
Db	1381	atcaacttaggaactgtacaacgcgacagcgaagatgtgagctgtgagacagaaatcttgg	1440
QY	1435	cccttataacatbgtgtgaagtlctgcgcacatccaagaagctccagaagtgtaacgcttcbg	1494
Db	1441	cccttataacatbgtgtgaagtlctgcgcacatccaagaagctccagaagtgtaacgcttcbg	1500
QY	1495	tgttcttggtgtgtgcgagacatacaattcttcagaagccgttttaactaaatggagact	1554
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QY	1555	atgagtgtgaaggtgcacttcaggtgtgaaacattcatgtgacgtgacggaanaacagagatt	1614
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QY	1615	gccaaagagacacccagagataltccgcgtgtaaatcttcgaattcaacttbatvggcaact	1674
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QY	1675	catcacccgaacttgaagaacacatattcttcagactcacacccacaaataaagaattcttc	1734
Db	1681	catcacccgaacttgaagaacacatattcttcagactcacacccacaaataaagaattcttc	1740
QY	1735	tcacctctctgaggtgtgcgaaaccttcagagaaacacttaacaagttcatcccttgac	1794
Db	1741	tcacctctctgaggtgtgcgaaaccttcagagaaacacttaacaagttcatcccttgac	1800
QY	1795	ttcaatccagtgatcttcgagagacttcggaagaaatgacgagacgaataacatgcaagaag	1854
Db	1801	ttcaatccagtgatcttcgagagacttcggaagaaatgacgagacgaataacatgcaagaag	1860
QY	1855	gagatgacacactccgttgggttactcaggtgcacataaagcccccctcgatttcccttgacaa	1914
Db	1861	gagatgacacactccgttgggttactcaggtgcacataaagcccccctcgatttcccttgacaa	1920
QY	1915	atgtgaacagagacacacagacttactactcgtgtgtaaatcttgtagtttcagcgtgtgagcat	1974
Db	1921	atgtgaacagagacacacagacttactactcgtgtgtaaatcttgtagtttcagcgtgtgagcat	1980
QY	1975	clagctgcacttaaacctgcclagaaacattatgacgaagacagacgagacgtgacgtcagcg	2034
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QY	2035	gaccttaacacagatataaagtataagcttccagagccctctgtccattatataagaatgac	2094
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QY	2095	tagccaacaaagtctcagaaagagacacatgacacgaagacagacagcctcaggtgtggccta	2154
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QY	3055	acaccccaagagccctggagcgtgtgtgacgcgcgtgtctcgtgcaccccaagagacagaanaa	3114
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QY	3115	ctctaaaggagatagtcaccaatgttgagagcccgccacatctgcgcgcacacattatgtgcttgg	3174
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Db	5641	tlagaaglatgclctcatagaacttlaaactlaaactaaagccttgtlaaanaactlcatgaa	5700
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QY	6115	atgtagaanaaaggtataatgtgaacactattctcatgtcagtagatatccttttgyt	6174
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QY	6955	aaagagagagagagcttcccccaacaacaatatttaatttctctgttaaaagataacag	7014
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QY	7195	cttttaatttcaatcaatttttttttcttccaaacagcaatagatagatcaactaaagca	7254
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QY	7615	gaattcatgatgattaggaatttctctccttlygaaaaggtctccctgtagtgaataat	7674
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QY	7735	tatatctaaatlyagcttggatcaacaacttlaagccagagccagctaaatgcgttccat	7794
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; Sequence 20, Application PC/TUS0032056
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Calferkey, Robert
; APPLICANT: Recipon, Hervé
; APPLICANT: Sun, Yongming
; APPLICANT: diadexus, Inc.
; TITLE OF INVENTION: A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING,
; FILE REFERENCE: IMAGING AND TREATING BREAST CANCER
; CURRENT APPLICATION NUMBER: PCT/US00/32056
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 60/166,973
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 10006
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US00-32056-20

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Query Match          96.5%; Score 9951; DB 1; Length 10006;
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? APPLICANT: Salceda, Susana
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? APPLICANT: Caffterkey, Robert
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? APPLICANT: Recipon, Herve
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? APPLICANT: Sun, Tongming
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? TITLE OF INVENTION: A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING
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? TITLE OF INVENTION: IMAGING AND TREATING BREAST CANCER
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? FILE REFERENCE: DEX-0117
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Query Match 65.7%; Score 6774.6; DB 1; Length 10246;
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Q	4502	caatbaatagaataggtttcttctgtatgtgaatcaatagcttgaatgtctttagag	4561
D	5840	CAATTAATTAAGAAATAGGTTTCTTGTATGGGAATTCATATGCTTGAATGCTTATGAG	5781
Q	4562	acctataaaaaactctatagagactgtccatataccaatgaaatccctctcttgg	4621
D	5780	ACCTATTTAAAAAATCTTATATAGACCCCTGCTTATCAACATGAATTCCTTTTGG	5721

QY	4622	ttatcttcttcttgtagttaggttcaacaga	cttaaaaaagagataaatggtcaatga	4681
Db	5720	TTATTTCTTTCTTTGATAGTAGTACGAT	TTAAAAGAGAGATTAATGTGTCATATA	5661
QY	4682	gaaagaaatggaatggttaaaacaaatca	ctttttaaaccgtgttaagttaaaacacattg	4741
Db	5660	GAAAAGATGCAAGATGCTAAACATTC	CTTTTAAAACTGTTAAGTCAAACATCTTG	5601
QY	4742	gctaatgtgactggggaaataaiaicaa	taagaagatactcaagactgaataataat	4801
Db	5600	GCTTAATGTGACTGGGGAAATPAITC	TAAGACATTCACACGAGCTGGAATTAAT	5541
QY	4802	tataaagaagaacccaacactgctcga	atttgaaaggttccatataataatactca	4861
Db	5540	TATAAATAAGAACCCAAACTGCTGCA	ATTGTAAGAGGGTTTACATTTATTAATCTAA	5481
QY	4862	agcagtactggaactggcaattggaaca	atttgttccaaaacccaataaatgttgtcca	4921
Db	5480	AGCAGTACTGGACTGGCATTGAGAC	ATTGTTGTCACCAAAACCATTAATGTGCTCAAA	5421
QY	4922	ttataatgatacatgaaacccctagc	acagaggaagaataatgaaggtccaggcaatgaa	4981
QY	4982	gaaaaatgagccctcccaatttgccttc	ccatgttcccatgtgccaatttccagatttga	5041
Db	5380	GAAATAATGGGGCCCTCTCATTTAG	TTCTTCTTCATGTGCCATGTTCACATTTTACCT	5301
QY	5042	agaaatgagagctgtgtgttaggtctgt	tagagtgcagcaagacacatgacagatgtgtg	5101
Db	5300	AGAAATGCGAGCTGNGGTTAGCTTG	TGGTGGAGTGCAGCAGCAACATGCACATGTGG	5241
QY	5102	caacgtgttttttaaccagccctgcctg	ctgttccaaacaaagacacacccctctga	5161
Db	5240	CACCGCTTTTAAACCAACCCCTGCCT	GTGTATPACATPACATPACATPACATPACATP	5181
QY	5162	gtcccttagatgttcaaatctacacag	tacagtcacctgttctgttcttgagttcaatctgtgc	5221
Db	5180	GTCCTTAGTGTTCAATACTCAGTAG	TGCTCTTTGTTGGGTTTGATTAATTTTGTC	5121
QY	5222	caacatgtcacccattcttaaaaaa	caaatgtccctgaagctctgttagtgaattcattta	5281
Db	5120	CACACATGTACCCATTTTAAAAA	CAATGCTCCGATCTCTGTAGTGAATTCATTTTA	5061
QY	5282	gcaaggtatttcttcttggtgtgtg	atgaaacaagatgagattgttcccttctcaagcctct	5341
Db	5060	GCCAGGTATTTCTTCTTGCTGTG	TGTCAGAACGATGTGATTTGCTTTTGTAAAGCTCTCT	5001
QY	5342	gttgttactaatccacttgcacattaa	ctaactaaagaatccctccaatcttaaaagca	5401
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QY	5402	tgaatggaatacaaatgtccaagcc	gcgtgtggttaattgtttgaacaacatgacattcttc	5461
Db	4940	TGAATGGAATCAAAATGTACAG	CCGTGGGTTTAATTTGTTTGAACACATGCACTTTCTTC	4881
QY	5462	acaaggttaacccgtgttatattat	tttcttcttggttaataataatttccaacattg	5521
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QY	5582	aatccctcaataaatgtatacaga	atttagttagcaatlaaatagattctctagaag	5641
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QY 5702 ctctcagataactgctcgaaggaatagggcctaataactgaacathtaataatigtgt 5761
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5762 aaagglgctgtaglccagcctcaagctgcttaccagaagatglatgtacaaagagctgact 5821
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Db 4580 AAACGTCGCTTACGCGACCCCAAGCTTCCGTAACAAGATGTATGTACAAAGCAGCTACT 4521
5822 ttaataattgcatatataatgctcccaacgaatgtatttttttgcgaaggaaatgtaga 5881
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Db 4520 TTAATAATTGCAATTAATATGTCACCAACGATGTTATTTTGGCCACGGAATGTAGA 4461
5882 agatataaagctactgagacgtctgagattactatttacttaagaagattggga 5941
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Db 4460 AGATATTAAACCTACTGAGACGCTCGATTAACCTTAATTTCAATTAAGAAAGTTGGA 4401
5942 gaacaaalaggaanaaaaaacttatttctttagtaaatataatglatatacttcaaa 6001
Db 4400 GAACAAATAGCAAAAAAACAATTTTCTAGTAATATTAATTAATTAATTAATTAATTA 4341
6002 taatgggctccacatallgaatlaattatttctacagtgtaagatagcaaaagatat 6061
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Db 4340 TAATGTCCTCCTACATATTGATTAATTAATTTCTACGCTGATGCAACAAAGATAT 4281
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Db 4280 TCCATCATGCAATTAAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4221
6122 aaacaaagatagaaagcaactatttctatttgcagtagalatccctttgtgtgtgtgt 6181
Db 4220 AAACAAGTAATGAAGCAACATTTTCTATGCTAGATATCTTTTGTGTGTGTGTGTGTGTG 4161
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Db 4160 TGCATTAAAGTTGTAAACGCTACATGAACAAATGAAGTCTTGCTGATTAAGATGATGG 4101
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6302 ttcaatcgaactttttttttttaaactttaagctcttaacacatgltatgtt 6361
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Db 3980 AAGATGATTAACATATATCTCTTTTATATGCTTTTGTCTATGTTCAATTAAGAAATTTT 3921
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Db 3740 GAGTTCAACCGT 3681
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Db 3260 GTTGGTAACTTGAGCAATATGCAAGTATTTCTTTTGGCAAAACCTGCTATTAAGC 3201
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7202 ttctcatcaatttttttttttctcagacagacatagatglatcaactagcatlgaag 7261
Db 3140 TTTTCATTAATTTTCTTTTCTTTTCTGACACGACATAGATGATGACATGACATGACATG 3081
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7502 atctcgaagataatataaatttacttcttcttcttcttcttcttcttcttcttcttctt 7561
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Db 2720 ATGATGATTTAGAAATTTCTCTTGGAAAGGCTTCCCTGATGAAGAAATGATGAGC 2661
7682 cagctaaatgt 7741
Db 2660 CAGCTAAATTTGT 2601
7742 taaattgagctllgatacaactttaggcagagacacatcgaatggcttcttcttcttctt 7801
Db 2600 TAAATTTGAGCTTTGATCAACCTTTAGCCAGACACACCTGATGCGTCTCAATTTTCT 2541
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Db 2540 TTTCTCACTCTTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2481
7862 atcataagagcaacacatcctcaagaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7921
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Qy	10082	taataatataatatataatag-----ag	10106
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Qy	10107	gcctcgtgaanigaatgggaaalcaaatcacattccaataaattactatatt	10166
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Qy	10167	galaaagccaggantctcctaacttglttgccttttcctttaaccaatcaac	10226
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Qy	10227	tcttaaccgatagatttggtaaaaagtataatctggtttctcagaagaattacaat	10286
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Qy	10287	aaaaatlglttatlalcaaaaaa	10311
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US-09-764-874-6816/c			
? Sequence 6816, Application US/09764874			
? GENERAL INFORMATION:			
? APPLICANT: Rosen et al.			
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
? FILE REFERENCE: PC010			
? CURRENT APPLICATION NUMBER: US/09/764,874			
? CURRENT FILING DATE: 2001-01-17			
? PRIOR APPLICATION NUMBER: 60/179,065			
? PRIOR FILING DATE: 2000-01-31			
? PRIOR APPLICATION NUMBER: 60/180,628			
? PRIOR FILING DATE: 2000-02-04			
? PRIOR APPLICATION NUMBER: 60/214,886			
? PRIOR FILING DATE: 2000-06-28			
? PRIOR APPLICATION NUMBER: 60/217,487			
? PRIOR FILING DATE: 2000-07-11			
? PRIOR APPLICATION NUMBER: 60/225,758			
? PRIOR FILING DATE: 2000-08-14			
? PRIOR APPLICATION NUMBER: 60/220,963			
? PRIOR FILING DATE: 2000-07-26			
? PRIOR APPLICATION NUMBER: 60/217,496			
? PRIOR FILING DATE: 2000-07-11			
? PRIOR APPLICATION NUMBER: 60/225,447			
? PRIOR FILING DATE: 2000-08-14			
? PRIOR APPLICATION NUMBER: 60/218,290			
? PRIOR FILING DATE: 2000-07-14			
? PRIOR APPLICATION NUMBER: 60/225,757			
? PRIOR FILING DATE: 2000-08-14			
? PRIOR APPLICATION NUMBER: 60/226,868			
? PRIOR FILING DATE: 2000-08-22			
? PRIOR APPLICATION NUMBER: 60/216,647			
? PRIOR FILING DATE: 2000-07-07			
? PRIOR APPLICATION NUMBER: 60/225,267			
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? PRIOR APPLICATION NUMBER: 60/251,869			
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? PRIOR APPLICATION NUMBER: 60/235,834			
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? PRIOR APPLICATION NUMBER: 60/234,274			
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? PRIOR FILING DATE: 2000-08-30			
? PRIOR APPLICATION NUMBER: 60/224,518			
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PRIOR APPLICATION NUMBER: 60/229,343			
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PRIOR APPLICATION NUMBER: 60/229,513			
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PRIOR APPLICATION NUMBER: 60/221,413			
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PRIOR APPLICATION NUMBER: 60/227,039			
PRIOR FILING DATE: 2000-10-02			
PRIOR APPLICATION NUMBER: 60/227,038			
PRIOR FILING			

1 PRIOR APPLICATION NUMBER: 60/225,213
2 PRIOR FILING DATE: 2000-08-14
3 PRIOR APPLICATION NUMBER: 60/227,182
4 PRIOR FILING DATE: 2000-08-22
5 PRIOR APPLICATION NUMBER: 60/225,214
6 PRIOR FILING DATE: 2000-08-14
7 PRIOR APPLICATION NUMBER: 60/235,836
8 PRIOR FILING DATE: 2000-09-27
9 PRIOR APPLICATION NUMBER: 60/230,438
10 PRIOR FILING DATE: 2000-09-06
11 PRIOR APPLICATION NUMBER: 60/215,135
12 PRIOR FILING DATE: 2000-06-30
13 PRIOR APPLICATION NUMBER: 60/225,266
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15 PRIOR APPLICATION NUMBER: 60/249,218
16 PRIOR FILING DATE: 2000-11-17
17 PRIOR APPLICATION NUMBER: 60/249,208
18 PRIOR FILING DATE: 2000-11-17
19 PRIOR APPLICATION NUMBER: 60/249,213
20 PRIOR FILING DATE: 2000-11-17
21 PRIOR APPLICATION NUMBER: 60/249,212
22 PRIOR FILING DATE: 2000-11-17
23 PRIOR APPLICATION NUMBER: 60/249,207
24 PRIOR FILING DATE: 2000-11-17
25 PRIOR APPLICATION NUMBER: 60/249,245
26 PRIOR FILING DATE: 2000-11-17
27 PRIOR APPLICATION NUMBER: 60/249,244
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37 PRIOR APPLICATION NUMBER: 60/249,214
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39 PRIOR APPLICATION NUMBER: 60/249,297
40 PRIOR FILING DATE: 2000-11-17
41 PRIOR APPLICATION NUMBER: 60/232,400
42 PRIOR FILING DATE: 2000-09-14
43 PRIOR APPLICATION NUMBER: 60/231,242
44 PRIOR FILING DATE: 2000-09-08
45 PRIOR APPLICATION NUMBER: 60/232,081
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57 PRIOR APPLICATION NUMBER: 60/232,397
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63 PRIOR APPLICATION NUMBER: 60/241,808
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65 PRIOR APPLICATION NUMBER: 60/241,826
66 PRIOR FILING DATE: 2000-10-20
67 PRIOR APPLICATION NUMBER: 60/241,786
68 PRIOR FILING DATE: 2000-10-20
69 PRIOR APPLICATION NUMBER: 60/241,221
70 PRIOR FILING DATE: 2000-10-20
71 PRIOR APPLICATION NUMBER: 60/246,475
72 PRIOR FILING DATE: 2000-11-08
73 PRIOR APPLICATION NUMBER: 60/231,243

1 PRIOR FILING DATE: 2000-09-08
2 PRIOR APPLICATION NUMBER: 60/233,065
3 PRIOR FILING DATE: 2000-09-14
4 PRIOR APPLICATION NUMBER: 60/232,398

Query Match 65.7%; Score 6774.6; DB 30; Length 10246;
Best Local Similarity 99.0%; Pred. No. 0;

Matches 6859; Conservative 0; Mismatches 26; Indels 40; Gaps 3;

1 QY 3422 gaccccaagcctttaacatcaataaacaacacggttgagcagatattagagagag 3481
2 Db 6920 GACCCCAAGCCTTTAAATCATTTAAACAAAACAGGTGACGATTTATAGAGAG 6861
3 QY 3482 aacaagaagcgcttaaccagagagacttcaggttgacgactcaacaacagcagag 3541
4 Db 6860 AACAAAGAAAGCGCTTAAACCCAGAGGCACTTCAGGCTGAGCAGCTCAACAAAGCAGAG 6801
5 QY 3542 ggggaagaatggagagcagatcaatgaaagccggttagagagaggttagaagatcatc 3601
6 Db 6800 GGGGAGCAATGAGAGCAAGCAATGGAAGCCGTTAGAGAGAGCTCAGAAATCATCT 6741
7 QY 3602 aactgaagtcacccagagagaattccaccccccagccttaagtaataagagccaggg 3661
8 Db 6740 AACTGAAAGTCACACAGAGAGAAATTTCCACCTCCAGCTTAAGTAATAGAGCCAGG 6681
9 QY 3662 ttaattgaactaaagacatctgctcagcagcagtcctgtgcagcacaactctgatat 3721
10 Db 6680 TTCAATTGACTAAAGACCTTCCTGCTCAGCAGCCAGCTGTCACACCAACTTGGATAT 6621
11 QY 3722 tccaaagaatgacacactttgcacatccagataaaagctccctcagagaagttactggag 3781
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13 QY 3782 tccaggaatagttatccglatctgaaaggaagaaattctggaagagcgatctat 3841
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17 QY 3902 aaagtaccagttaccacttttgacttcccttgtaataatgactccaagtgaaag 3961
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19 QY 3962 tgaattgcgctgctgagtaataataagctccgctctggaagtcagcactat 4021
20 Db 6380 TGAATTGCGCTGCGTTCTGGAGTAAATTAAGCTTCCTGCTGGAATCCGCACTACT 6321
21 QY 4022 gagtcagtgctggtgctcaaatctctgcacaaactatgtgccttatccacactcaa 4081
22 Db 6320 GAGTCAGTGCTGCGCTGACCAATCTTGCMAAATGATGCTTATCCCACTTCAA 6261
23 QY 4082 tctgctctcacttttttagctgttgatcagaatgacatccctctagatttggagat 4141
24 Db 6260 TCTGCTCCTCATTTTTCAGCTGTGATCAGCAATGCAATTCCTTAATTTGGCGAT 6201
25 QY 4142 caagcattccagacctgggccaactgcaacggtgtccccaagagagaacagagcacc 4201
26 Db 6200 CAAGCATTCACACCTGGGCGCAACTGCAAAAGCGTCTCCAAAGGAGAAACGAGCACC 6141
27 QY 4202 accaaatgtaaaaaatagaaggtcccttgaatgtagtaaaaaacagagaagttagaag 4261
28 Db 6140 ACCAAATGTAAAAATGAAGGTCCCTTGATGTATTAATAACAGAAAGTATATGAG 6081
29 QY 4262 tactcaagaatgaacttcaaaaaatgtgtgcaactgtggcatgtcttctggaatgaag 4321
30 Db 6080 TACTCAAGATGACTTTAAACAAATGTGTGCACTGTGGCAATGTCTTTTGATTAAGT 6021
31 QY 4322 gatgtatgttgcataatgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatg 4381
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QY 4382 ccagacatcttgcagcgacaatatagctaccacaacatalccagaaggccctgcatag 4441
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Db 5360 CCGACATCTTGCACGCGACAATATGACTTCACAAACATATCCAGAGGGCCCTGCATAG 5901
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Sequence 6816, Application US/10092400		
GENERAL INFORMATION:		
APPLICANT: Rosen et al.		
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PRIOR APPLICATION NUMBER: 60/214,886		
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PRIOR APPLICATION NUMBER: 60/217,487		
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PRIOR APPLICATION NUMBER: 60/233,065

Query Match Best Local Similarity 65.7%; Score 6774.6; DB 37; Length 10246;
Matches 6859; Conservative 0; Mismatches 26; Indels 40; Gaps 3;

QY 3422 gactccagagcctttaacalcaataacacaacaggttagcagatttagagagag 3481
DB 6920 GACTCCAGAGCCTTTAAACATCATTAACAAAACAGCGTAGCAGATTATTAGAGAG 6861
QY 3482 aaaaagaaagagccttaacccaagagcacttagcgttagcagctcaacaacagagag 3541
DB 6660 AACAAAGAGAGCCTTTAAACCAAGAGGACTTCAAGCTGAGCAGCTCAACAAAGAGAG 6801
QY 3542 gggcagcaatgagagcaatgaatgaagccggttagagagagaggttcagaaatcatct 3601
DB 6800 GCGCACAGCAATGAGAGCAATGCAATGGAAGCCCGTTAGAGAGAGGCTGAGAAATCATCT 6741
QY 3602 aactgaagtlcaccagagagaaatlccactcccgagcctaagtaaatgaagccagag 3661
DB 6740 AACTGAAGTCAACAGAGAGAAATTCACCTCCCGAGCTTAAGTAATAGCAAGCCAGAG 6681
QY 3662 ttcatgtctaaagcattctcttagagagccagctcctgttgcagccaactcttgatat 3721
DB 6680 TTCAATGACTAAAGGCAATCTCTGAGAGGCACTCCTGCTGAGCAAACTTTGGATAT 6621
QY 3722 tcacaaagagatgaacatttgacattcagataaagttccctcaggaagatcagagag 3781
DB 6620 TCACAAAGAGATGCAACCTTTGACATTCAGTAATAAGTCTTAGGAAAGTACTGAGA 6561
QY 3782 tccaggaataagtlcatccgtalcgtgaagggaaagagagttctgaaagagagagctcat 3841
DB 6560 TCCAGGAATAGTTCATCCGTATCTGAAAGGAAAGAGTTCAGAGAGGCAAGTCTAT 6501
QY 3842 agaaagatgagagagcctgagaaagcccaaatattatccacccagcagccctattga 3901
DB 6500 AAAAAAGTACATGAGAGCTGCGAAMACCAAAATTAATTCACACAGGAGCCCTATTGA 6441
QY 3902 aaagtaacagtaacacattttgagctcccttgatcaataagacttcagagagagagc 3961
DB 6440 AAAGTACAGTACCACTTTTGGAACTTCCCTTGTACATAAATGACTTCCAGAGTGAAGC 6381
QY 3962 tgattgctgaggttctggaataaataaagctccgcttccctggaagatccgactactt 4021
DB 6380 TGATTTGCTGCGGTTTGGAGTAATAATATAGCTCCCTTTCGGAATCCGCACTACTAT 6321
QY 4022 gagtaagtgctgagcctacaaatcccttgccaaactatgtccttatcccaactca 4081
DB 6320 GAGTACGTGCTGAGCTTACCAAACTCTTGGCAAAATATGATGCTTATCCACCTTCAA 6261
QY 4082 tctgacctcatattttcagctgttgaatcagacaagacatccctcagagagagagat 4141
DB 6260 TCTGCTGCTGCTGCTTTCAGCTGTGAGTACAGAAATGACATCTCTTATGATTTGGCAT 6201
QY 4142 caagcaltccagacctgggccaactgcaaacgtgtcctccaagagaaacagagagacc 4201

DB 6200 CAACCATTCAGACCTGGGCCAACTGCAAAAGGTGCTCCAGAGAGAAAAGAGAGAC 6141
QY 4202 accaaatgttaaaaaatgaaggtcccttgatgtagtaaaacagagaaagttgataag 4261
DB 6140 ACCAAATGTAAAAATGAAAGGTCCCTGAATGTGTAATAAGAGAAAGTGTATGAAG 6081
QY 4262 taaccaagatgaacttcaacaaaatgtgtcacctgtgacattgtcttcttgatgaag 4321
DB 6080 TACCAAGATGAACTTCAACAAAATGTGTGCACTGTGGCATTTGCTTGTGCAATGAG 6021
QY 4322 gatgatgcttgcatatgaatltgcaatgtgcaatgtgacattccagtgcaagatag 4381
DB 6020 GATGTATGCTTTGCAATGATGATGTCATGCTGATGATGATGATGATGATGATG 5961
QY 4382 ccagcctcttgcaagagcaataatgaacttcaacacatccagagagagagagatag 4441
DB 5960 CCAGCATCTTTGCAAGGAGCAAAATGTGCTTCAACAACTGCAAGAGGAGCTGATAG 5901
QY 4442 gaacaatgacaagltggaaaaaatggaaaacctgaaggttaaaacttgcagcttagca 4501
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DB 5840 CAATTAATTAAGAAATAGGTTTCTTGTGATGGGAATTCATAGCTGTATGATGATGAAG 5781
QY 4562 acctataaaaaatcacttcagagcctgagccttatccaaatgaatccctctcttg 4621
DB 5780 ACCTATTAATAAATATCTCATAGAGCTGCTTATCCAACTAAATTCCTCTTTTGG 5721
QY 4622 tatlcttcttltgatlgaatgaatltacaagattaaaggtgagatlaaagtgatga 4681
DB 5720 TTATCTTTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5661
QY 4682 gaaagatggaagatggttgaacaaatcaacttlttaaacctgttgaatcaaacacatctg 4741
DB 5660 GAAAGATGGAAGAGTGAATGAATCACTTTTAAACCTGTATGAGCAAAACATCTTG 5601
QY 4742 gctaatatgactggggaataatccataagagatatccagagctgaaatattatatt 4801
DB 5600 GCTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5541
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DB 5540 TATTAAGAAAGAGAGCAAAACTGTGATGATGATGATGATGATGATGATGATGAT 5481
QY 4862 agcagactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4921
DB 5480 AGCAGTACTGAGAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGCAGTGGC 5421
QY 4922 ttataatgatcatgaaccccttagagagagagagagagagagagagagagagagag 4981
DB 5420 TTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5361
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DB 5300 AAAAAATGGAAGCTGTGATGAGCTGTGATGAGTGAAGAGCAAGAGCAAGATGAGTGG 5241
QY 5102 cagcgtgttttaacagcgcctgcctgctgataacagcagcagcagcagcagcagcag 5161
DB 5240 CAGCGTGTTTTACCAAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGAT 5181
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QY	6362	aagatgataaacatataatccctctttaa	gtctgtgctatgattcaca	tgaaacattc	6421
Db	3960	AAGATGATAAACATATATCCCTTTTA	AGCTTTATAGCTTTGTCTAAGTTGCATATGAACAATTC	3921	
QY	6442	agaatatatttggataagtgctgtggaac	ctgcaagcgcattttttt	tgattcttcgt	6481
Db	3920	AGAAATATTTTGGATATAGTGTTCGT	GTGAACCTGCAACGCTGATTTTTTTT	TGCATTCCT	3861
QY	6482	agtcgaatttgcattccatttttaccat	taatttcgaagtttgcatttctgtt	ctgatttctgt	6541
Db	3860	AGTCGATTTGCACTCCATTTTNCAT	TATATGCAAGTTGCTTTGTATCATATGTTTCT	3801	
QY	6542	tgggttttcttctcttccacaagtgc	cgcggtcttcgtttctaagt	ttggaatgcagta	6601
Db	3800	TGGGTTTGTTCCTTTTCCACAGTCC	GGGCTCTCGTTCTTTAAAGTTGATGGCAGTA	3741	
QY	6602	gaatcaacaacgatttgcactgtgtg	aggaatgaagttaaaaaatgcttctc	gtaagt	6661
Db	3740	GAGTTCAACCGAGTGTGACGTTGT	AGCAATGAAGATTTAAAAAATGCTTCGATGT	3681	
QY	6662	tgtgttgcatttccatttccatttgc	atttcttctgttgcatactaaaaaag	agaagaaga	6721
Db	3680	TGTGTTGTCAATTTTCATTTTGCAT	TTTTTTTGTTCATATTTAAAAAACAAGAAAGCA	3621	
QY	6722	aagcaagagacagaatacagaacta	agctccctgcctcgaattccattcatt	ctgttaacgagcct	6781
Db	3620	AAGCAAGACACGAATATCAGCACT	ATATCCTCGTTCAGTTTCATTTGTTAAAGGCGCT	3561	
QY	6782	attctgatctaacctgtcggtgagct	ctataattccataacacgcgaataaga	aaagtga	6841
Db	3560	ATTCTGATCTCACCGTGTCCGTAC	CTCTTAATTTACATTAACGAATTAACAAATGTGA	3501	
QY	6842	atgaaggagcttgcattccaatattg	atgatacttaattcttccttagaact	atttgaatg	6901
Db	3500	ATGAGAGAGCTTTGACATTCAAAT	TATGTGATGTGAATTTATCTTCCTTAGAATTTTGATG	3441	
QY	6902	gatgcattccaaatgataagcaga	cttgagaggtgagcaataaagatc	taaaaaaag	6961
Db	3440	GATGCATCTCAAAATGTATACCA	GACTGTGAGAGGTGACATTTAAATATCTAAAAAGG	3381	
QY	6962	aggagaattcccccacaaacaaat	atttaattctctagtataaaaaga	atacagaatgcatt	7021
Db	3380	AGGAGATTTCCCCCAACACATAT	TTTAATTTTAACTTAAAAAGAAATTAACAATATCAT	3321	
QY	7022	ctgtggaacacctgaagcaacatt	atcatctgtgagcttctaactcag	caaaaacacagaa	7081
Db	3320	CGTGGCAATCCTTAGCAACATTAT	CTATCTGTGAGCTGCTTAAATACGCAAAACACCAACA	3261	
QY	7082	gtttgtttaaacttggcgaata	atgacaagratctctt	ttggcgaacaaactcattacgc	7141
Db	3260	GTTTGTGTAACTTGGGCAATAT	GCAGATTAATTTTGGCAAAATCATATTAAGC	3201	
QY	7142	aatttctcagagtggttgcgaca	aaataagttcttatttctt	tttggcatgatagccttcta	7201
Db	3200	AATTTTCTAGAGTGTGTGGACACA	AAATAGGTCCTTAATTTTGGCATATGATGCTTTTGA	3141	
QY	7202	tttttccatcaatttttttttttct	cagaacagacatagatgatac	aaacagatttggaa	7261
Db	3140	TTTTTCATTCAAATTTTTTTTTTTT	CTCAGACACACATAGTACTATCANCTATAGATTTGGAAA	3081	
QY	7262	atacatatacactattcttgaata	attatgtctcagctctcattt	ttgtatgaataattcttg	7321
Db	3080	ATTCATATCATACATTTTGGAAAT	TTATTTAGTGCATCTTTTATAGTAAATATTTTGTG	3021	
QY	7322	gataaggttgacaagatagatct	atccatacctcttattatgata	atttattcttc	7381
Db	3020	GATAGGTTTGACGCATAGATTCAT	TATTCACATCTTTATATATATATTAATTTTATTTTC	2961	
QY	7382	atttttcttccattatctataac	attcttctgttgagaaagaggt	ttggcctcttttggaa	7441
Db	2960	ATTTTTCCTTCATATATATATAT	TTTGTGTGAGAAAGGCTTGCGCTTTTGTGGAAG	2901	

Db	1820	TAAGTTGAGAGAGGCTAAATTACTACTCTCTTGTTGAGAGCCATGGCAAAAAA	1761
QY	8582	aaaaaagaaaaaagatcaagtcgcctcttggtagccagtaaggtgaaagcttbcgact	8641
Db	1760	AAAAAAGAAAAAAGATCAAGGTCGCTTTGGTAGGCAAGATAGGTGAAGCTTGCCTACT	1701
QY	8642	gtccaaagccacaagagaaaaattgagaaatgaaatgcaacctgagtcatacctaataat	8701
Db	1700	GTTCGAAGCCACACAGAAATAATTGAGGAATGTGAATGCAACTGAGTATCAAACTAAATAT	1641
QY	8702	tctaatcaaggtgagtgactcgtttagtggaattcttatcgccagcggaactgcaatagaa	8761
Db	1640	TCTTAATCAAAGCTTAGGTAAGTACTGTACGTGGAATTCATCAAGCAGCACTGCAATGAGAA	1581
QY	8762	gaagataagagaagccgcctcgaggactttgagaggaattgatttcccaagaaagac	8821
Db	1580	GAAAGATAGAAGAGAGCCCTCGGAGCTTTGGAGGCACTTGTTATTTTCCAAAGAAAGAC	1521
QY	8822	gtccaaagggcagaagggcattgattcttgcagaggaactcctttggttttcagtaact	8881
Db	1520	GGCCAAAGGGAGAGGAGCATGGATTTCTTTCAGAGCACTCTCTTTGTGTTTTCAGTACTCT	1461
QY	8882	ttcatagagcgttggtgcacatggttcctctgtagtgcctcagttgcttagaagacatccca	8941
Db	1460	TTCATAGCAGATGGGCTCCACATGTTCCGTAAGTGGTGCAGTTGGTTAGAAACATCCCA	1401
QY	8942	gttaattgcagtaatatagaactcttgcgaatcgtcggcagaagatgctgaagatgctc	9001
Db	1400	GTTTAATGCGATTAATTAGAACTTCCTGGCAATATCTAGGGCAAAAGTATGTCAAGTATGTC	1341
QY	9002	aaatgaagaaatgtaaatcccaagagtaatccacacgltgagaactagacaaatgtaacat	9061
Db	1340	ACATGAAGAAAAAGTAAATTCAGAGATTAATCCACAGCGAAGAAACTAGACATGTACAT	1281
QY	9062	tcaatgtctctcttgaagagaagggagcgtgtaagcttaaccctgctctcaaccggag	9121
Db	1280	TCACTGTCTCTGTTGAAGAGAAAGGAGACGTGTAAGCTTCACATCTGCTCAACCGGAG	1221
QY	9122	aaaagcagaataacttaccgttgaataatglttagcttcttatacagagaanaattgctc	9181
Db	1220	AAAAGCAGGAATPACTTTACCGTGGAAATATGTTTACGTTTATCCAGAAAAATGTGTC	1161
QY	9182	ttctaagggcatagagttcccaaaactcaatctcgtgtttcccccgttttttttttttttt	9241
Db	1160	TTTCTAGAGCATAGAGTCCCAAAACTCAATCTGTGGTTTTCCCTGTTTTTTTTTTTTTTT	1101
QY	9242	tttcccaacataatgaactgtagcatatacaactttcttctttgtgctcaaggtctccac	9301
Db	1100	TTTTTCCACATATGACATCGACCATATPACATTTTCTTTTGTGCTCAGAGTCTCTCCAC	1041
QY	9302	ctgtaaaatlgaaaaataatcgtatataaatatattataataataataatgtaatgtag	9361
Db	1040	CTGTAAAAATTTGAAAAATATATGATTAATATATATATTTAAATATATATGTAATGTAG	981
QY	9362	tactcgtttgttaagcactttgagatcccttgtgtgaagggaccataaggagtgccaagta	9421
Db	980	TACTGTGTTTGTAAMCATTGTAGATCTCTGGTTGAAGGACCATATGAGGTGCCAAGTA	921
QY	9422	ttattatgtagcgaagggggtttttaaacgtcagttcccaaaagccagaagagtttg	9481
Db	920	TTTATTTATGTGGCCAAAGGGGGTTATTTAAACCTGTCAGTTCCCAAAAGGCCAGAAAGTGG	861
QY	9482	gttcatcttcttctaagaagcagctgtaaatcaaatcaggcagacaaatagtggtgactat	9541
Db	860	GCHCATTTTTTCTTTAAAGCAGACTGTAAATATATCAAACTATGGGACCAATATGTTGTACAT	801
QY	9542	gaagatgcaaaaacttacttagctgctgatataaatcatatagtttcttaagtccacaataag	9601
Db	800	GAAAGATGCAAAACTATTAAGCTCATTAATAATATATAGTTTCTTAATGGCTTACCAATAG	741
QY	9602	gcaaatatcacaaataataaacgcccaattcctttagggcggaactattgacaacacattgg	9661

1	PRIOR FILING DATE: 2000-07-11	
2	PRIOR APPLICATION NUMBER: 60/225,444	
3	PRIOR FILING DATE: 2000-08-14	
4	PRIOR APPLICATION NUMBER: 60/218,290	
5	PRIOR FILING DATE: 2000-07-14	
6	PRIOR APPLICATION NUMBER: 60/225,755	
7	PRIOR FILING DATE: 2000-08-14	
8	PRIOR APPLICATION NUMBER: 60/226,866	
9	PRIOR FILING DATE: 2000-08-22	
10	PRIOR APPLICATION NUMBER: 60/216,644	
11	PRIOR FILING DATE: 2000-07-07	
12	PRIOR APPLICATION NUMBER: 60/225,267	
13	PRIOR FILING DATE: 2000-08-14	
14	PRIOR APPLICATION NUMBER: 60/216,880	
15	PRIOR FILING DATE: 2000-07-07	
16	PRIOR APPLICATION NUMBER: 60/225,270	
17	PRIOR FILING DATE: 2000-08-14	
18	PRIOR APPLICATION NUMBER: 60/251,865	
19	PRIOR FILING DATE: 2000-12-08	
20	PRIOR APPLICATION NUMBER: 60/235,833	
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22	PRIOR APPLICATION NUMBER: 60/228,922	
23	PRIOR FILING DATE: 2000-08-30	
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26	PRIOR APPLICATION NUMBER: 60/236,365	
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32	PRIOR APPLICATION NUMBER: 60/241,809	
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34	PRIOR APPLICATION NUMBER: 60/249,299	
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36	PRIOR APPLICATION NUMBER: 60/236,327	
37	PRIOR FILING DATE: 2000-09-29	
38	PRIOR APPLICATION NUMBER: 60/241,785	
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48	PRIOR APPLICATION NUMBER: 60/251,868	
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50	PRIOR APPLICATION NUMBER: 60/229,344	
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53	PRIOR FILING DATE: 2000-09-25	
54	PRIOR APPLICATION NUMBER: 60/229,343	
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56	PRIOR APPLICATION NUMBER: 60/229,345	
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58	PRIOR APPLICATION NUMBER: 60/229,287	
59	PRIOR FILING DATE: 2000-09-01	
60	PRIOR APPLICATION NUMBER: 60/229,513	
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62	PRIOR APPLICATION NUMBER: 60/231,413	
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68	PRIOR APPLICATION NUMBER: 60/237,039	
69	PRIOR FILING DATE: 2000-10-02	

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? PRIOR FILING DATE: 2000-09-14
? PRIOR APPLICATION NUMBER: 60/232,398

Query Match      63.9%; Score 6587.2; DB 1; Length 10004;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 6657; Conservative 0; Mismatches 13; Indels 12; Gaps 5;

QY 3422 gactccagagccttaaacatcatlaaacaaacacggttagacagatlaagagagag 3481
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DB 6619 AACAGAAAGGCGCTTAACCCAGAGGCACTTCAGGCTGAGAGCTCAACAAACAGAGAG 6560
QY 3542 gggcagcaatgagagcaagtaaatgaagagccggttagagagagaggttcagatcct 3601
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DB 6439 TTCATTGACTAAAGCCATTCTCTCAGAGCAGCACTCTGTGTCAGCCAAACTCTGATAT 6380
QY 3722 tcacaaagagatgcacacttgacacatcagataaagaagtcctcagaagaagtcggaga 3781
DB 6379 TCACAAAGAGATGCAACCTTTCGACATTCAGATTAAGAAAGTCTCTGAGAAAGTCTGAGA 6320
QY 3782 tccaggaataatgctcactcgtalcgtgaaggaagagagtcctgaagagagagccat 3841
DB 6319 TCCAGGAATAATGTTCACTCCGTATCTGAGGGAAGGAAGTTCTGAGAGGAGGAGTCTAT 6260
QY 3842 agaaagagacagagcctgagcagaaacaccccaatatatccacacagcagccctatga 3901
DB 6259 AGAAAGAGACAGAGCCTGAGCAGAAACACCAATATATTCACACAGGAGCCCTATGGA 6200
QY 3902 aaagtagcagtagccacttttgagactcccttgtaacataagacttcacagagtagagc 3961
DB 6200 AAAGTAGCAGTAGCCACTTTTGAGACTCCCTTGTAACATAAGACTTCACAGAGTAGAGC 3961
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Db	6199	AAAGTACCAAGTACCCACTTTTGGACTTCCCTTTGTAACAAATGACTTCCAGAGTAAGC	6140
Qy	3962	tgatcgtctgaggtctctgagtaataataagctctccgtctccctggagatccgacactt	4021
Db	6139	TCATTGSGCTGGGGTCTGSGAGTAATATAAGCTCTCCGTCTCTGGGAATCCGACTACTT	6080
Qy	4022	gagtcagctgcctgcgcctacccaatccctgcgcaaatctatgctctatccacactcaa	4081
Db	6079	GAGTACGCTGCTGGGCGCTACCAAAATCCCTTCCAAAACATGTGCGCTTATCCGACTTCA	6020
Qy	4082	ctctgcctccctcaatlltttaagcgttgtatataagcaatgcacatccctctagattggcat	4141
Db	6019	TCGTCTCTCATATTTTTCACGTGTTGGATAGCAATGACATTCCTCTACATTTGGCAT	5960
Qy	4142	caagatcttcaagacctgggccaactgcgcaaacggtgcctccagaagaagaagcgacc	4201
Db	5959	CAGAGTTCACAGACTGGGCGCACTGCAAAGCGTGCTTCOAAGSAGAAACGAGGCAAC	5900
Qy	4202	accaaatgtaaaaatgaaaggtcccttgaatgtrgtaaaaaagagaagttgatagaag	4261
Db	5899	ACCAAAAGTAAAAAATGAAGGTCCTTGAATGTAGTAATAAACAGAGAAATGTATAGAG	5840
Qy	4262	laccagaatgaaacttcaacaaaatgttgcactgtggcctgtctcttcgtatgaaat	4321
Db	5839	TACTCAAGATGAACCTTTCACAAATAATGTGCACTGTGGCAATGTCTTCTGTGATGAGAT	5780
Qy	4322	gattatgccttcgatalatagaatctgcaatgtgtacaagtgagaccttccaatgtagaatgt	4381
Db	5779	GATGTATGCTTTGCATATGATTTGCGATGCTGACAGTGGACCTTTCAGTGCAGATATG	5720
Qy	4382	ccagcatctttgcacggaacaaatagtactccaacacatatccagagggcgctcagat	4441
Db	5719	CCAGCATCTTTGACGGGCAAAATGTGACTTCCAAACATATCCAGAGGGGCGCTGCATAG	5660
Qy	4442	gaacaaatgcgaagtggaaaaaaatgaaaaccttaagatgaaaaaccttaagactlagca	4501
Db	5659	GAACTAATGCAACAGTGTGAAAAAATGTGAAAAACCTTAAGATGAACCTTATGCACTTAACA	5600
Qy	4502	caactaatlagaataataggtttctcttgatggaaatcaatagctgtgaatcttctatagaag	4561
Db	5599	CAATTAATATGAAATAGGTTTCTTGATGTGGAAATTCATATAGCTTGTATAGCTTATGAG	5540
Qy	4562	acctataaaaaaactactcatagagcgctgcctatcccaactgaaatccctctcttg	4621
Db	5539	ACCTATATAAAAAATCTCTCATAGAGCGCTGTATCCAAATGAATATTCCTCTTTTG	5480
Qy	4622	ttatctctctctttaaagaagagttacaaagatatlaaagaatgaagatgaataaatgctcatga	4681
Db	5419	GAAAGAAATGAGATGATGTAATCAATCATCTTTTAAACCTGTTTAACTCAAAACATCTTG	5560
Qy	4742	gctaatatgtactggggaataatcatataagatatcatocagacactagaataatataatc	4801
Db	5359	GCTAATATGCTACTGGGAAATATTCATATAGATATACCAAGATACAGATTAATATATAT	5500
Qy	4802	tataaagaagaagaagccaacactctcagaatttlaaagggttlaatatatatactaa	4861
Db	5299	TATTAAGAAAGAGACCAAACTGTCTGAGATTTTAAAGCGTTTACATATTTATTTACTTAA	5240
Qy	4862	agcagtaactgagcctgagcatcttgacacatttgttcaaacaccotaatatttgttctaata	4921
Db	5259	AGCAGTACTGACGGCGCATTTGACCATTTGTTCAAAACCCATTAATTTGTGCTTAAAT	5180
Qy	4922	tataatgtcatataaaccttagcagagagaggaatgaaggttccagggcaataaa	4981
Db	5179	TTATATGATCATATAAACCTTAGCGAGAGAGGAATATGAAGGTCCAGGGCATATGAA	5120
Qy	4982	gaaaatgagcgccctccaattagtctctctcatatggcagatgttccaattggacct	5041
Db	5119	GAAAAATGGCGCCTCATATTTAGCTCTCTCTCATATTTGCGGCAATGTTCCAGTTTGGACCT	5060

QY	5042	agaatgcgagctcgttgtaggtcgtgtgtagagtgagcaagaacgaacgaatgcagatgtagc	5101
Db	5059	AGAAATGGAGAGCTGTGGTTAGSCTTGGTTAGAGTGGAGAGCAACAAACATGACAATGGTG	5000
QY	5102	caacgtgtttttcccaagccctgcgtctaatacacatgcaacccctctctgtatlttt	5161
Db	4999	CAACCGCTGTTTTACCCAGCCCGCCTGGACATFACACATGCACACACGCTCGATTTTTTTT	4940
QY	5162	gtcccttagaagtgtaaatgaacgaagtagtccctttgtttgggtttagatlttcgtc	5221
Db	4939	GTCCCTTAGATGTTCAAAATACGATGAGTCGTCCTTTTGTTCGGCTTTAGATTCATTTTGTGC	4880
QY	5222	cacacatgtaaccattttaaaaaaacaatgtccctcgatgtctctgtagatgttcatttta	5281
Db	4879	CACACATGTGCCATTTTAAAAACAATGTCCCTCGATGCTTGTGAGTGAATTCATTTTAA	4820
QY	5282	gccaggtattcttcttctgtgtgtgtagaacaagtagatgtattgtcttctaagcctct	5341
Db	4819	GCCAGGATTTTTCTTCTGTGTGTGATGAACACAGTATGAGATTGGTTTGTTTAAAGCCTCT	4760
QY	5342	gttggttaacaaactcactcttgagacattataactaagaagaaicccctcaatltcaaaaga	5401
Db	4755	GTTGCTTACATAACTACTCTGGCACATTTAATACGTAAAGAAATCCCTCAATTTCAAAAGCA	4700
QY	5402	tagaatgatacaaatgtcaagacgctgggttaattgttttgaagacatgtagatcttc	5461
Db	4659	TAGATGATACAAATGTCAAGTCCAGACCGTGGTTTAATTTGTTAGAACAAATGGCAATTCTTC	4640
QY	5462	acaaggtaacctgcgtgtagattattatttctttgtgttaataaataatcccaacttg	5521
Db	4639	ACAAGGTAACTCCGCTGATTTTATTTATTTATTTCTTTGGTTAAATTAATTTCCAAAGTTTG	4580
QY	5522	tggtcgaagcagctctaaggttaagtgtaacaaagacgaacgctgtgatactgtaccaccc	5581
Db	4579	TGCTCAAGCAGCGCTCAAGAGTTACGTTACCAAGACTACAGCTGGTGTATATGACCAACC	4520
QY	5582	aatccctcaataatgatacaaatgattgaatgaatgacataaataagattcctaaga	5641
Db	4519	AATCCCTCATTAATGATFACAAATTTAGTTAGTACATTAATATGATTCCTTAGAG	4460
QY	5642	tatgtcctaatagaaccttaactaactaaagcttgttaaaacatlocatgaaaggaag	5701
Db	4459	TATGTCCATATFAGAACTTTTAATACCTTAAGCGTTGTGAAACATATCATGAAAGGAAG	4400
QY	5702	ctccgaagataaagctcctcagaagaaataggcttaataaiaacgaacatlaaataatgct	5761
Db	4399	CTCCTCAAGATTAACGTCTCAGGGAATFAGCGGTAAATFACGAACATTTAAATTAATTTGGTT	4340
QY	5762	aaagtgctgttagtcgagccctcaatgctgtctcaagaagatgtaatgtaagaagtagct	5821
Db	4339	AAAGTGCTGTAGTACGAGCCTCAATGCTTGCTCAAAAGATGTTGTAACAAGAGCTGACT	4280
QY	5822	ttaataattgcatatatattgtgccacaacagtagtattttttggccagagatgtaga	5881
Db	4219	TTAATAATTTTGCAATTAATTTGTCCCAACACAGTAGTTTATTTTGGCCAGGAGATGTAGA	4220
QY	5882	agatattacaagctcagatgtagaagcgtgaagttactatttcaatlaaagaagtggga	5941
Db	4219	AGATATTAAACCTACTGGATGACGTGCAGATTAACCTATTTCATTAAAGAAAGTTGGCA	4160
QY	5942	gaacaaatagaaaaaanaaactatctttctcagaatataatgaatgatatlaacttaaa	6001
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QY	6002	taatgtgcctgacataatgaataattatltctacagtgtagttagcaaaagaat	6061
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QY	6062	tcaatataacatgaatgaatgcttgcctcgtcgtgactagcgtttaacttgcgaatgtagc	6121
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QY 8161 gtagaagcgttggtagacattatgttaataatgacatgtagcaataactattatg 8220
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QY	9413	tgccaagatattatattgtgcgaagggggatttaaacctgcagttccccaaggccagg	9472
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Db	620	AAAGGTTTGGGGTCATTTTCTTTAAAGCGCGCTGTAATATCAACTAGGAGCCAAATAGT	561
QY	9533	gttactactagaagatgcaaacacttaactcagggtgatataaactagtttcttaatgct	9592
Db	560	GTTGACTATGAAAGATGCAAAACTTTACTAGGCTGATTTAAATCTATGTTTCTTAATGGCT	501
QY	9533	accaataagggcaaatatcacaaataaagaogccaaatlcctlaagggcgacatttgaca	9652
Db	500	ACCAATAAGGCAAAATATCACATATTATPAAGGCCAAATTCCTTAGCGGGGCTATTGGACA	441
QY	9653	accaacttggaaaacttttggggggagcattgaaggggggaacatctcaaatgccaatgttaa	9712
Db	440	ACCACTATGAAAACTTTTGGGGAGCGCATGAGGGGGAAATCTCAAAATGCCAAATGTAAA	381
QY	9713	attaacttaccagcaatatctaccagcaagaatgtcttcttaatatgtaatgttttcagt	9772
Db	380	ATTAACTTACGACATATTCTACACGACAAAATGCTCTTTATATGGAATGATTCATGT	321
QY	9773	tgtctagaaaaaagaacttcaatttqtagtctcgtatgtgaactagaatgttgcataat	9832
Db	320	TGCTAAGAAAAAGAAATTCAAATTTCTAGTCCCTGATTTGCAATACATGATGCTATAT	261
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Db	260	AGTTCTGTTCTTACACACATGAAATTTTTCGGTTTATTTTATTTTGGTTTCATATGTC	201
QY	9893	atgttcaattctactcacaacaactgtctcttggctgtattcttcttaagcaacaactctagg	9952
Db	200	ATGTCATTTTACTACACAACAAATGTTCTGGTGATTTCTTAGCAAACTCTTAGG	141
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QY	10013	aacggctgttgatagtggttatgatgtacttcaacttcaactcactcaggcaataggaataac	10073
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US-09-764-874-6814/c			
: Sequence 6814, Application US/09764874			
: GENERAL INFORMATION:			
: APPLICANT: Rosen et al.			
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
: FILE REFERENCE: PC010			
: CURRENT APPLICATION NUMBER: US/09764, 874			
: PRIORITY FILING DATE: 2001-01-17			
: PRIORITY APPLICATION NUMBER: 60/179, 065			
: PRIORITY FILING DATE: 2000-01-31			
: PRIORITY APPLICATION NUMBER: 60/180, 628			
: PRIORITY FILING DATE: 2000-02-04			
: PRIORITY APPLICATION NUMBER: 60/214, 886			
: PRIORITY FILING DATE: 2000-06-28			
: PRIORITY APPLICATION NUMBER: 60/217, 487			
: PRIORITY FILING DATE: 2000-07-11			
: PRIORITY APPLICATION NUMBER: 60/225, 758			
: PRIORITY FILING DATE: 2000-08-14			
: PRIORITY APPLICATION NUMBER: 60/220, 963			
: PRIORITY FILING DATE: 2000-07-26			
: PRIORITY APPLICATION NUMBER: 60/217, 496			
: PRIORITY FILING DATE: 2000-07-11			

1	PRIOR APPLICATION NUMBER: 60/225,447
2	PRIOR FILING DATE: 2000-08-14
3	PRIOR APPLICATION NUMBER: 60/218,290
4	PRIOR FILING DATE: 2000-07-14
5	PRIOR APPLICATION NUMBER: 60/225,757
6	PRIOR FILING DATE: 2000-08-14
7	PRIOR APPLICATION NUMBER: 60/226,868
8	PRIOR FILING DATE: 2000-08-22
9	PRIOR APPLICATION NUMBER: 60/216,647
10	PRIOR FILING DATE: 2000-07-07
11	PRIOR APPLICATION NUMBER: 60/225,267
12	PRIOR FILING DATE: 2000-08-14
13	PRIOR APPLICATION NUMBER: 60/216,880
14	PRIOR FILING DATE: 2000-07-07
15	PRIOR APPLICATION NUMBER: 60/225,270
16	PRIOR FILING DATE: 2000-08-14
17	PRIOR APPLICATION NUMBER: 60/251,869
18	PRIOR FILING DATE: 2000-12-08
19	PRIOR APPLICATION NUMBER: 60/235,834
20	PRIOR FILING DATE: 2000-09-27
21	PRIOR APPLICATION NUMBER: 60/234,274
22	PRIOR FILING DATE: 2000-09-21
23	PRIOR APPLICATION NUMBER: 60/234,223
24	PRIOR FILING DATE: 2000-09-21
25	PRIOR APPLICATION NUMBER: 60/228,924
26	PRIOR FILING DATE: 2000-08-30
27	PRIOR APPLICATION NUMBER: 60/224,518
28	PRIOR FILING DATE: 2000-08-14
29	PRIOR APPLICATION NUMBER: 60/236,369
30	PRIOR FILING DATE: 2000-09-29
31	PRIOR APPLICATION NUMBER: 60/224,519
32	PRIOR FILING DATE: 2000-08-14
33	PRIOR APPLICATION NUMBER: 60/220,964
34	PRIOR FILING DATE: 2000-07-26
35	PRIOR APPLICATION NUMBER: 60/241,809
36	PRIOR FILING DATE: 2000-10-20
37	PRIOR APPLICATION NUMBER: 60/249,299
38	PRIOR FILING DATE: 2000-11-17
39	PRIOR APPLICATION NUMBER: 60/236,327
40	PRIOR FILING DATE: 2000-09-29
41	PRIOR APPLICATION NUMBER: 60/241,785
42	PRIOR FILING DATE: 2000-10-20
43	PRIOR APPLICATION NUMBER: 60/244,617
44	PRIOR FILING DATE: 2000-11-01
45	PRIOR APPLICATION NUMBER: 60/225,268
46	PRIOR FILING DATE: 2000-08-14
47	PRIOR APPLICATION NUMBER: 60/236,368
48	PRIOR FILING DATE: 2000-09-29
49	PRIOR APPLICATION NUMBER: 60/225,856
50	PRIOR FILING DATE: 2000-12-08
51	PRIOR APPLICATION NUMBER: 60/225,868
52	PRIOR FILING DATE: 2000-12-08
53	PRIOR APPLICATION NUMBER: 60/229,344
54	PRIOR FILING DATE: 2000-09-01
55	PRIOR APPLICATION NUMBER: 60/234,997
56	PRIOR FILING DATE: 2000-09-25
57	PRIOR APPLICATION NUMBER: 60/229,343
58	PRIOR FILING DATE: 2000-09-01
59	PRIOR APPLICATION NUMBER: 60/229,345
60	PRIOR FILING DATE: 2000-09-01
61	PRIOR APPLICATION NUMBER: 60/229,287
62	PRIOR FILING DATE: 2000-09-01
63	PRIOR APPLICATION NUMBER: 60/229,513
64	PRIOR FILING DATE: 2000-09-05
65	PRIOR APPLICATION NUMBER: 60/221,413
66	PRIOR FILING DATE: 2000-09-08
67	PRIOR APPLICATION NUMBER: 60/229,509
68	PRIOR FILING DATE: 2000-09-05
69	PRIOR APPLICATION NUMBER: 60/236,367
70	PRIOR FILING DATE: 2000-09-29
71	PRIOR APPLICATION NUMBER: 60/237,039
72	PRIOR FILING DATE: 2000-10-02
73	PRIOR APPLICATION NUMBER: 60/237,038
74	PRIOR FILING DATE: 2000-10-02
75	PRIOR APPLICATION NUMBER: 60/236,370
76	PRIOR FILING DATE: 2000-09-29
77	PRIOR APPLICATION NUMBER: 60/236,802
78	PRIOR FILING DATE: 2000-10-02
79	PRIOR APPLICATION NUMBER: 60/237,037
80	PRIOR FILING DATE: 2000-10-02
81	PRIOR APPLICATION NUMBER: 60/237,040
82	PRIOR FILING DATE: 2000-10-02
83	PRIOR APPLICATION NUMBER: 60/240,960
84	PRIOR FILING DATE: 2000-10-20
85	PRIOR APPLICATION NUMBER: 60/239,935
86	PRIOR FILING DATE: 2000-10-13
87	PRIOR APPLICATION NUMBER: 60/239,937
88	PRIOR FILING DATE: 2000-10-13
89	PRIOR APPLICATION NUMBER: 60/241,767
90	PRIOR FILING DATE: 2000-10-20
91	PRIOR APPLICATION NUMBER: 60/246,474
92	PRIOR FILING DATE: 2000-11-08
93	PRIOR APPLICATION NUMBER: 60/246,532
94	PRIOR FILING DATE: 2000-11-08
95	PRIOR APPLICATION NUMBER: 60/249,216
96	PRIOR FILING DATE: 2000-11-17
97	PRIOR APPLICATION NUMBER: 60/249,210
98	PRIOR FILING DATE: 2000-11-17
99	PRIOR APPLICATION NUMBER: 60/226,661
100	PRIOR FILING DATE: 2000-08-22
101	PRIOR APPLICATION NUMBER: 60/225,759
102	PRIOR FILING DATE: 2000-08-14
103	PRIOR APPLICATION NUMBER: 60/225,213
104	PRIOR FILING DATE: 2000-08-14
105	PRIOR APPLICATION NUMBER: 60/227,182
106	PRIOR FILING DATE: 2000-08-22
107	PRIOR APPLICATION NUMBER: 60/225,214
108	PRIOR FILING DATE: 2000-08-14
109	PRIOR APPLICATION NUMBER: 60/225,836
110	PRIOR FILING DATE: 2000-09-27
111	PRIOR APPLICATION NUMBER: 60/230,438
112	PRIOR FILING DATE: 2000-09-06
113	PRIOR APPLICATION NUMBER: 60/215,135
114	PRIOR FILING DATE: 2000-06-30
115	PRIOR APPLICATION NUMBER: 60/225,266
116	PRIOR FILING DATE: 2000-08-14
117	PRIOR APPLICATION NUMBER: 60/249,218
118	PRIOR FILING DATE: 2000-11-17
119	PRIOR APPLICATION NUMBER: 60/249,208
120	PRIOR FILING DATE: 2000-11-17
121	PRIOR APPLICATION NUMBER: 60/249,213
122	PRIOR FILING DATE: 2000-

Query Match	63.98;	Score 6587.2;	DB 30;	Length 10004;
Best Local Similarity	99.68;	Pred. No. 0;		
Matches 6657; Conservative	0;	Mismatches 13;	Indels 12;	Gaps 5

6199 AAGTACCAGTACCCACTTTTGGACTTCCTTGTACATAATGACTTCCAGAGTGAAGC 6140

QY	3962	tgattgctgcgglltctggtgtaataataagctcccglltccgggaatccgcactactt	4021
Db	6139	tgattggctggcggtctctggagtaaaafatnaacctctccggtctcgggaaftccgcactactt	6080
QY	4022	gagtaagtcgcctggscgtaccaaactccctggcaaaactatgctctatcccaacttca	4081
Db	6079	gagttacgtgctggccttcttccaaattccctggcaaaactatgctctatcccaacttca	6020
QY	4082	ctcgctccctcaatttcttagcgtgtgtgatcaagaataaactcccttaggtttggcga	4144
Db	6019	tcggccttcctcatttttcaacgctgttggaatcaacaattacattcccttngatttggcga	5960
QY	4142	caagcatlccagacgctggtccaactgccaacggtgcctccaagagagaaacgaagacac	4201
Db	5959	caagcatlccagacgctggtccaactgccaacggtgcctccaagagagaaacgaagacac	5900
QY	4202	accgaatgtaaaaaaagaagtccttcccttgaaatgtatgaataacagaaatltgataga	4261
Db	5899	accgaatgtaaaaaaagaagtccttcccttgaaatgtatgaataacagaaatltgataga	5840
QY	4262	tactcaagatgaaacttcaacaaatgtgtgaacgtgtgacgttcttccttgatgaagt	4322
Db	5839	tgctcaagaatgaaacttcaacaataatgtgtgaacgtgtgacgttcttccttgatgaagt	5780
QY	4322	gattgtatgcttgcataatgagtltgcaatgtgtgacagtgtgacgttccctcagtgcaagatg	4381
Db	5779	gattgtatgcttgcataatgaaacttcccatgctgacgtgacgttccctcagtcacacatg	5720
QY	4382	ccagatccttlttgacggacaataatgtactccaacacataatccagaagggctgcatag	4441
Db	5719	ccagatccttlttgacggacaataatgtactccaacacacatccagaagggctgcatag	5660
QY	4442	gaacaatgacaaggtgtgaaaaaatgtgaaacactgaagtgaaaccttgacgttga	4501
Db	5659	gaacaatgacaaggtgtgaaaaaatgtgaaacacttgaaagtgaaaccttgacgttga	5600
QY	4502	caatlaaatgaataatgagtttctcttgatgtgaatcaatagcttgaatgctctatgaag	4561
Db	5599	caattaaatgaaatgagtttctcttgatgtgaatcaatagcttgaatgctctatgaag	5540
QY	4562	acctatlaaaaaaatactctatagagctgccttaccacatgaaatccctctcttg	4621
Db	5539	acctatlaaaaaaatactctatagagctgccttaccacatgaaatccctctcttg	5480
QY	4622	ttatctctcttcttgatgtagaggtttaccaagaattgaagaatgagaataatggtcaata	4681
Db	5479	ttatctctcttcttgatgtagaggtttaccaagaattgaagaatgagaataatggtcaata	5420
QY	4682	gaagaatgtgaagatgtgtlaaacaatcaacttlaaaacctgtlaagccaacaacatctg	4741
Db	5419	gaaagaatgtgaagatgtgtlaaacaatcaacttlaaaacctgtlaagccaacaacatctg	5360
QY	4742	gctaattgtacatgggggaataatcacaataagagataccacagactagaattatattt	4801
Db	5359	gctaattgtacatgggggaataatcacaataagagataccacagactagaattatattt	5300
QY	4802	tataaagaagaagacaaataatgtctcagaattgaaaggtttacataattatattacaa	4861
Db	5299	tataaagaagaagacaaataatgtctcagaattgaaaggtttacataattatattacaa	5240
QY	4862	agcagctacgtgacgtgacatltgttccaacaacccaataattgttgcctaaat	4921
Db	5239	agcagctacgtgacgtgacatltgttccaacaacccaataattgttgcctaaat	5180
QY	4922	ttataatgatacatalgaacccataggacagagggaggaataatggaagtcagggcaatga	4981
Db	5179	ttataatgatacatalgaacccataggacagagggaggaataatggaagtcagggcaatga	5120
QY	4982	gaaataatgggcctcctaattatgactcttcctcattgttgacatggtttgaagctttga	5041
Db	5119	gaaataatgggcctcctaattatgactcttcctcattgttgacatggtttgaagctttga	5060

QY 5042 agaaatgagagctggtggttaggtgtagagtcgacgaacaaatgacagatggtg 5101
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Db 5059 AGAAATCCAGAGCTGGGTAGAGCTGGTGAAGTGCAGCAACAAATGATGATG 5000
QY 5102 caagctgttttaccacagccctgctgtacacacacagacacccctcgtatatttt 5161
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Db 4999 CAAGCTGTTTTACCAGCCCTGCCCTGAATACACATGCAACCCCTCTGATATTTT 4940
QY 5152 gtcccttagatgtlcaaaactacagtagtcccttcttggcggttagattcttgc 5221
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Db 4939 GTCCTTAGATGTCAAAATACAGTACAGTCTTTGTGTGGGTTCATTCATTTTGC 4880
QY 5222 cacacatgacccattttaaataaacaatgtcctgagtcctcgttagtgattcatt 5281
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Db 4879 CACACATGATGCCATTTTAAAAACAATGTCTCCAGTCTCTGATGATTCATTTTA 4820
QY 5282 gccaggtattcttcttctgtgtgtgtgtagaaccaagatgatttcttcttctaagctcct 5341
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Db 4819 GCCAGGTATTTCTTTCTGTGTGTGATGAAACAGATGATGATTTCTTTTAAAGCTCTCT 4760
QY 5342 gttggttactaatctacatctgacacatlaaactaaagaaatccctcaattlcaaaaga 5401
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Db 4759 GTTGTACTATCTACCTATGCGACATTAATTAAGTAAGATCCCTCATTTCAAAAGCA 4700
QY 5402 taagatgatacaaaatgtcagacccgtgtgtgttaatttctttagaacaatgacattcttc 5461
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Db 4699 TAAATGGATACAAATATGTAACCGTGGTAAATTTGTTTGAACAATGSCATTTCTTC 4640
QY 5462 acaaggtacacccgtgctatttatttcttcttgggttaataatcttccaactttg 5521
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Db 4639 ACAAGTAAACCGGTATTTATTTATTTCTTTGTTAAATTAATTTCCAAACTTTTG 4580
QY 5522 tggtaagcagcgtctaaagttlaagtlacacacagactgacagttggtataglacagcc 5581
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Db 4579 TGGTCAAGCAGCGCTCAAGGTACGTACCAACAGACTGACAGTTGATATGTACAGCC 4520
QY 5582 aatccctcaattaaatgtatagagattttagttagtcataatagagattccttaaga 5641
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Db 4519 AATCCCTTCATTTAAATGTATACAGATTTAGTAAATGACATTAATTAATGATTTCTTAAG 4460
QY 5642 tatgtccatagaaactttaaactaaagcttgtlaaaactatccatggaaggaag 5701
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Db 4459 TATGTCTCATAGAACTTTTAAATTAAGCTTTGTAAACATTCATTCATGAAAGGAAG 4400
QY 5702 ctccctcaacaaactgtcaggaagaaatagagctaaactgaacatlaaataattgtt 5761
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Db 4399 CTCCTCAACATTAACCTGCTCAGGGAATAGGGTAAATTAACGAACTTAATTAATTTGTT 4340
QY 5762 aaagtgctgttagtcagagcccaatgctgtgtgtaagaagtgatatacaagagctgact 5821
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Db 4339 AAAGTGCTGTAGTACAGCCTCAATGCTGTCTCAAGGATGTATGTACAAAGACTGACT 4280
QY 5822 ttaataatttgcatlataatgtlcccaaccagtagttatttcttgccagagagatgaga 5881
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Db 4279 TTAATAATTTGATATTAATTTGCCAACACAGTAAATTTTGGCAGGAGATGTAGA 4220
QY 5882 aagatatacaagctactgagatgacactgtcagaatlaactatttcaatlaaagaattgaga 5941
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Db 4219 AATATTTACAAAGCTACTGATGACTGTCAATTAATTAATTTCAATTAAGAGTTGGA 4160
QY 5942 gaacaaatagaaataaacttatttcttagtaataactaaatgattatattacattcaaa 6001
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Db 4159 GAAACAAATAGGAAAAAAATCTTTTCTTCTAGTAAATTAATTAATTTTCAATTTTCAA 4100
QY 6002 taatgtgtcctgacatattgaataatttctttagacagtgatcatcaacaagaattat 6061
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Db 4099 TAAATGTGCTGACATTAATTAATTTTCAAGTGTACAGTATGCAACAAAGATAT 4040
QY 6062 tcaatagatgaatgaatgatttctgtgctgtgctgactgatttacaatttgcaatgtgagc 6121
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Db 4039 TCCATCATGATTAAGATGATGTGCTGTGCTAGCTGTATTAATTTGCAAAATGTAGC 3980
QY 6122 aaacaaggtatgaagcaactatttctatgtcagtagatatacttctgtgtgtgtgtg 6181

Db 3979 AAAACAAGTATGAACACATTAATTTCTATTGCGAGTGAATATCTTTGTGTGTGTGTG 3920
QY 6182 tgcattaaagtgtlaaagcgtlaaactgaacaaatgaagttcttgcataatgataag 6241
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Db 3919 TGCAATTAAGTGTAAAGCGTAAACATGAACAAATGAAGTCTTGCTATTAATGTATGG 3860
QY 6242 aaacaagaagaagaatgaanaatatttctatgctacttagaanaaaaggttagaccta 6301
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Db 3859 AAAACAAGGAAGAAATGAATAATTTTATGCTACTATGGAAGAAAAAGGCTACACTTA 3800
QY 6302 ttcattccaagtacttt 6361
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Db 3799 TTGATTCGAAGTACCTTTTCTTTTAAATTTTAAACCTCTTAACACATGATTAATGCTT 3740
QY 6362 aagatgataaatalatcccttcttatttgccttgccttgccttgccttgccttgccttgc 6421
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Db 3739 AAGATGATTAACATTAATTCCTTTTATTTGCTTTGCTATGATTAATGAACATTTTC 3680
QY 6422 agaaattatttgaataagttgtgtgtaacatgcaacgtgat-tttttttgacttgcg 6480
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Db 3679 AGAAATTAATTTGATTAAGTGTGCTGGAATCTCAACGCTGATGTTTCTTGTGATTCG 3620
QY 6481 tagtcgacttgcactccatattttaaacttaattcgcagttcgttgcataatgtttgt 6540
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Db 3619 TATGCCATTTCACTCCATTTTACATTAATTCGACAGTGTGCTTGTATCATTTGTTTGT 3560
QY 6541 ttgggtttgttcttcttccaaagtgccgggtcttgccttgccttgccttgccttgccttgc 6600
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Db 3559 TTGGTGTGTTGTTTCTTTTCAACATGCGCGTCTTCTGTTTCTTAAGTGTGATGCGAGGT 3500
QY 6601 aaggttcaacacgctcgtgactgtctgtagcgaatgaatlaaanaaaatgtcttctgag 6660
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Db 3499 AGAGTCAACCAAGTGTGAGTGTGAGGATGAAGTAAAAAATGTCTTCTGAG 3440
QY 6661 ttgtgtgtcatttcaatttcttgcatttcttgcatttcttgcatttcttgcatttcttgcatt 6720
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Db 3439 TTGTGTGTGATTTTCAATTTTGTGATTTTGTGTGATTTTGTGATTTTGTGATTTTGTG 3380
QY 6721 aaagcaagagacaaatcaaggaactagtccttgccttgcatttgcatttgcatttgcatt 6780
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Db 3379 AAAGCAAGAGACAAATACAGAGCTAAGTCTGCTGCTTCACTTGTGATTAACGGCT 3320
QY 6781 tatttgcattcactgttgcgttagctcttaattcacaataaactgaataaagaattgag 6840
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Db 3319 TATCTGATCTACCTTACAGCGTACGCTCAATTAATTAATTAATTAATTAATTAATTAAT 3260
QY 6841 aatgagagacttgcattcaaatatgtgtagtaatttcttcttgcatttgcatttgcatt 6900
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Db 3259 AATGAGAGACTTTGACATTAATTTATGATGATTAATTTATCTTCTTACGAAATTTTAT 3200
QY 6901 ggaatcattcnaaatgtatagcgaactgagaggtgacatlaaagaatcnaaaaga 6960
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Db 3199 GATGCAATCTCAAAATGTATAGCCAGCTGAGAGGTGACATTAATTAAGATTAAGAA 3140
QY 6961 gaggagattccccaacaaatatttatttctttagtaaaagaataaagaatgaga 7020
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Db 3139 GAGGAGATTTCCCAAAACAATTAATTTATTTCTTAAAGAAATTAAGCAATGCA 3080
QY 7021 tctgtgcaatccttaagcaactatcraatgtgtagcgttaatacaagaacaaacga 7080
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Db 3079 TCGTGGCAATCTTAAACAAATTAATCTATGATGATGATGATGATGATGATGATGATGAT 3020
QY 7081 agttgtgttaacttgggcaatagcaagtalacttcttgggcaaaactactactaag 7140
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Db 3019 ACTTTGTGTTACTTGGGCAATATGACAGTATTAATTTTGGGCAAACTACTGATTAAG 2960
QY 7141 caatttcttagtggtgtggaacaaacaggttcttatttggcagatgagctttt 7200
|||||
Db 2955 CAATTTCTTAGTGTGCGACAAATAGGTTTATTTATTTTGTGATGTAGCCTTTT 2900
QY 7201 atttcaatcaatttcttctcagacagcatagatgaatcaactgacttgaa 7260
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Db	2899	ATTTCATCAATATTTTTTTTTTTTCTCAGACACACACTAGTACATGACATGACATTTGGAA	2844
QY	7261	AATCAATCAACATCTCTGTAATATTAAGTCACGTCACCTTTAGTAAATATTTT	7320
Db	2839	AATACATATCATTCTTGGAAATATTTATGGTCACCTACTTTTATGATATTTTTT	2780
QY	7321	ggataagcgttgcacagatagatcctatccactccttattatlatgatlatlta	7380
Db	2779	GGATACGGTTGACACATGATGATCTTAAATTCACCTCTTAAATATGATATTTATTTT	2720
QY	7381	catttttgccttcattatatacaatcttttggtagagaaggttggccttttga	7440
Db	2719	CATTTTGGTTTCATATATTAACATATTTTGGTGAGAAAGGTTGGCTTTTGGAA	2660
QY	7441	gagacaaattatatacaactaacactccttttggacatataagccttatct	7500
Db	2659	GAGACAAAAATTTATTTATTAACACTAAACACTCTTTTGGACATATTAAGCCCTTAATTC	2600
QY	7501	catctctcaagatataataataatlaatttlttaattlaagattctgaattatla	7560
Db	2559	CATCTCAGAGATATATTAATAATTAATTTTAAATTAATTAAGATTTGCAATATATTTTA	2540
QY	7561	tcttaaatgttgattttaaagagagactatagtgaagaaactttttaaaggaa	7620
Db	2539	TCTTAATTTGTGATTTTAAAGACATATTTGGTAGAGAAAGGTTGGCTTTTGGAA	2480
QY	7621	catgatatttaggaattctctcttgagaagagctcccttgtagtaaaatgctg	7680
Db	2479	CATCATATTTTAAAGAAATTTCTCTTTGGAAAGCTTCCCTGTGATGAATAATGTGTG	2420
QY	7681	ccagctlaaaattgtgtgccattlaaanaactlgaanaalattlaaattatgtctat	7740
Db	2419	CCACCTTAAATTTGTGCCATTTTAAACCTGAAAAATTTTAAATTTTGTGATATTT	2360
QY	7741	ctaatttggagtttggatccaacttaaggcagagacagcctcatggtctcatctcc	7800
Db	2359	CTAATTTGACCTTTGGATCAAACTTTTAAAGCAGACAGCTCATGCGCTTCTCATCTTCC	2300
QY	7801	ttctctacacttctctccacactaacccctgctatcatctctgttttggataga	7860
Db	2259	TTTTTCTACCTTTCTCTCATCACTCACTCACTCTGTATTTATTTCTGTGTGGATGA	2240
QY	7861	aatcaataaagccaaacccatctcagaacgtltggaattgagatgagacatcaatg	7920
Db	2239	AATCATTAAGACCCAAACCATCTCAAGACGTTGTGATTTGAGAGACACTCATGACTTC	2180
QY	7921	caagttatgaaanaagagacagagcctctaattgataactctgtatgtcaaaagaa	7980
Db	2179	CAGATATATGAAAAAGGACAGAGCTCTAATTTGATTAACCTGTATGAAAGGAAAGA	2120
QY	7981	gta tggccaattctctcaactagacatcttgagatcttttatacacttttaagat	8040
Db	2119	GTAATGCCAATTTCTCTCACTACACTATGACATTTTGAGATTTTTPAATCAACTTTTAAGAT	2060
QY	8041	tgatgttcgttcttaaacgtgtcctgttcttagtgaagylagatlttataaacaagc	8100
Db	2059	TGATGTTCTGCTTAACTGCTCTGTTTTAAAGAGAGATTTTAAACAGCATG	2000
QY	8101	ggagatctctttctaagtgtaataataatggaaggggaaaaaagatccttaacagc	8160
Db	1999	GGGATCTTTTCTAAAGATATTAATTAATTAAGGAGGAAAAAGATATCTTTAAACAGCTCTT	1940
QY	8161	gttgaagcctgtgtgtagacattatgttataatgtgacatgtgacataactatgt	8220
Db	1939	GTTGAAGCCTGTGTGACACATTTATTTATTTTGCACATGTGCACATTAATCTATTTATG	1880
QY	8221	atccaaatgcaaatcacgctcccaaaaataaaatgataatgataatlaaagcctg	8280
Db	1879	ATCCAAATGCAAAATACAGCTCCAAAAATATTAAGTATATATTTTAAATAGCTGAG	1820
QY	8281	aaatacaatcttcttataaactcgaagagctcgaatgtgctataaataatattagc	8340
Db	1819	AATATATATTTTCTTAATAAACGAGAGACTCTGAGTGTGGCTTTTAAATATATTTATG	1760

QY	8341	ctctcgtctgtgtgctgcgcaaaacatccaaagtgcacggtctttagaccctgtgaactgct	8400
DB	1759	CTCCTGTGTGTGGCTGCGAAAAACATCACAAGTACG - CTCGTGACACCTGTGANTGCT	1701
QY	8401	gccctgttagtaataataaattaatgcatcttcagagggggaatatctgcacacagctg	8460
DB	1700	GCCCTGTTAGTAATAATAAATAATGATTCCTAGAGGGGAGAAATCTGCATCCAGTGG	1641
QY	8461	tggaaatgttgagtaaaagaacctggtgtctgtctgtgtgcctatgcacgacctttgc	8520
DB	1640	TGGAATGTGTGATTAAGAACCTGTGTGTGCTGCTGTGTGTGTGATCCAGCCCTTTTGC	1581
QY	8521	ttaagttgaagagagtcacacttttagctactgtctgttttggtagacatgcac - aaaa	8579
DB	1580	TTAAGTTGAAGAGAGTCACACTTTTAGCTACTGTTTGGTTTGGAGACCATGGCAAAAA	1521
QY	8580	aaaaaaaaaanaaagaalcaagtcgtcttggtagccagtaagtgaaagctgttcga	8639
DB	1520	AAAAAAAAAAGAAAAAGATCAAGTCGCTTGGTGGTGCAGTAAAGTGAAGTGTGCA	1451
QY	8640	ctgtccagagcgcaagaagaataattggagaattggaatgcaactgagatcaactaat	8699
DB	1460	CTGTCCAGGCGCACAGACAAAAATTGAAGATTTGAATCCAACTCGATCAACAACATAAT	1401
QY	8700	attctaacaaggttaagttactgttgaagtggaattctatacagaggaactcaaatag	8759
DB	1400	ATTCTAATCAAGGTAGAGTACTGTTAGTGTGCAATTCATCCAGCGCACTGCAATATAG	1341
QY	8760	aagaagatgaagaagcgcgcctcgagacttggaggagcatgttatcttccaaagaag	8819
DB	1340	AAGAGATGTGAAGAGCGCGCCCTCGAGCACTTGAGAGCGCAGTTATTTCCAAAAAG	1281
QY	8820	acggccaaggcggaagsgatgagatctctttgcagagcaactcctcttgyttttcagact	8879
DB	1280	ACGGCCAAAGGCGAGGAGATGTGATCTTTTGCAGACACCTTCCTTTGTGTTTCAGTACT	1221
QY	8880	gtttcatalagacaggtgggtcacatgtcttcctgtagtgctgaagttcttagaaacatcc	8939
DB	1220	GTTTCAATACAGTGTGGGCTGCATGTTTCTCGATAGTGCTGCAGTGTGTAGAAACATCC	1161
QY	8940	caagttaatgcaagtaattagaactcttgaaatagctagagcgagaagtagtgcagatg	8999
DB	1160	CAGTAAATTGCAGTAAATTAGAACTTCGGAATATCTGAGCGAGAAAGTATGTCAGTATG	1101
QY	9000	tcacatgaagaanaatggaatctcaagtagtaatccacgctgagaaactagacaatgac	9059
DB	1100	TCAATGAAGAAAAATGTAAATTCAGAGATATCCACGCTGAGAAACATGACATGTAC	1041
QY	9060	attcatgttctctcttgaagaagaaggagcgttaagcttaaccctctccataccgg	9119
DB	1040	ATTCAATGTCTCTCTTGAAGGAAAGGAGACCTTAAAGCTTCACTCTGTCTTACACCG	981
QY	9120	agaaaagcagaataacttaacctgaagtggaataaagtcttaagcttttatacagagaanaatgt	9179
DB	980	AGAAAAGCAGAAATACCTTAACGTGTGAATATATGTTAGCTTTTATCGAAGAAAAATGT	921
QY	9180	cccttcagagcatagagctcccaaaactcaatctcggtttccctg - - - - - tttctt	9232
DB	920	CCCTTCAGAGCATAGAGTCCCAAAATCATATCTGTGTTTCCCTCTTTTTTTTTTTT	861
QY	9233	ttttttttttttccacaatatgaactcagaacatcacacttttcttttggctccag	9292
DB	860	TTTTTTTTTTTTTCCCAACATAGAACTGCACCAATATCTCTTTCTTTTGTGTGCACG	801
QY	9293	gtttccaccctgtgaatatgaanaatatgtatataataatataatataatg	9352
DB	800	GTTCCCTCAGCTGTAAATGTAATAAATATATGATTAATATATATATATATATATATG	741
QY	9353	gtaaagtacactgtttgttaagaacatttgaatccctgtttgaaaggcaccatagag	9412
DB	740	GTAATGTATGATCTGTTTGTGAAGCACTTTAGATCTCTGTTGAAGGCACATAGAG	681

QY 9413 tgcgaagatattatgtgccaaggggttattaaactgtcagttcccaagccagg 9472
DB 680 TGCCAGATATATATGTCGCAAGGGGTTATTATTAAGTGTGCTCCCAAGGCCAGG 621
QY 9473 aaaggttggttcaatttcttaagaagcgtctaaatatactagcagccaaagt 9532
DB 620 AAAGGTGGGTCATTTTCTTAAGACGAGCTGTAAATATCACTAGCCCAATAGT 561
QY 9533 gttgactatgaagatgcaaacctttactagagctgaataatcaatgttcttaagct 9592
DB 560 GTTGACTATGAAGATGCAAAACATTAAGCTATAGGCTATAAATCACTAGTTCTTAAGGCT 501
QY 9593 accaataagccaatatcatcaataaagccaaatcccttaaggagagctttgaa 9652
DB 500 ACCAATAAGCCAAATATCAATATTAACGCCAAATTCCTTAGGGCGACTTTTGACA 441
QY 9653 accaataagaaaactttgaggagagcalgaagggggaacatctcaaatcccaatgaa 9712
DB 440 ACCACATGCAAAACCTTGGGGGAGCATGAGGGGGAACATCTCAAAATCCCAATGTAA 381
QY 9713 atttaacttaagcaatattcaccagcagaataatgtcttcaataggaatgtatcagt 9772
DB 380 ATTAACTTACGCAATATTAATCCAGCAAGAAATGTCTTTCATATGGAATGATTCAGT 321
QY 9773 tgcgaagaaagaatcaattgtatgctcgtattgatactaggaatgttgcatat 9832
DB 320 TGCTAGAAAAAGATTCATTTGTAGTCTCTATTTGAATACATGATGTTGCTATAT 261
QY 9833 agtctgtcttaacacacatgaacttttcttatttatttcttcttcttagagtc 9892
DB 260 ACTGTGTTCTTACACACATGAATTTTTCGTTTATTTTATTTTGTTCATAGTCC 201
QY 9893 atgtcatttctactcaaacatgtcttctgttatttcttcttcttcttcttctcagg 9952
DB 200 ATGTTCAATTTTACTCTACAAACATGTCTGTGTATTTCTTATGCAAAACATCTTCAGG 141
QY 9953 cagcaagaatgtctgttacatctaaactgaataaagtttaccacattccaat 10012
DB 140 CAGCAAAAGATGTGTGTACATCAAACTGATATTAAGTTTACACCAAGTTCACAT 81
QY 10013 aacggcgttgatggttattatgattcacttccactcctcttagcagaatgaataac 10072
DB 80 AAGCGCGTGTATGTTTATGATTCACCTTCATTCCTCTAG--CATATGCAATAC 23
QY 10073 agalcatgtatataatata 10094
DB 22 AGATCATTTGTAATATATATA 1

RESULT 12
US-10-092-400-6814/c
Sequence 6814, Application US/10092400
GENERAL INFORMATION:
APPLICANT: rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC010CI
CURRENT APPLICATION NUMBER: US/10/092,400
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
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8	PRIOR APPLICATION NUMBER:	60/231,244
9	PRIOR FILING DATE:	2000-09-08
10	PRIOR APPLICATION NUMBER:	60/233,066
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12	PRIOR APPLICATION NUMBER:	60/233,063
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16	PRIOR APPLICATION NUMBER:	60/232,399
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24	PRIOR APPLICATION NUMBER:	60/241,786
25	PRIOR FILING DATE:	2000-10-20
26	PRIOR APPLICATION NUMBER:	60/241,221
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28	PRIOR APPLICATION NUMBER:	60/246,475
29	PRIOR FILING DATE:	2000-11-08
30	PRIOR APPLICATION NUMBER:	60/231,243
31	PRIOR FILING DATE:	2000-09-08
32	PRIOR APPLICATION NUMBER:	60/233,065

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OY	3482	aaacagaagcgcccttaaccacagagcgacttcagctgtgaagctcaacaacaagagag	3541
Db	6619	AACAGAAGGCCCTTAAACCCAGAGCGCACTTCAGCTGAGCGTCAACAAACAGCAGAG	6566
OY	3542	gagcgacgaatgagggagcaagccaatggaagcccgctttaagagagagfcaagaatcatt	3601
Db	6559	GGCGACCATGAGAGGCAAGTCAATGSAACCCGTTAAAGAGAGAGGTCAAAATATATT	6500
OY	3602	aactgaagtcacacagagagaatcttcactcccccagctcaagtaatacgaagcccaag	3661
Db	6499	AACGTGAATCTCCAGAGAGAAATTCACATCCCGCCAGCCCTAAGTAAATACAAACCCAGG	6440
OY	3662	ttaattgaactaaagacattctgtctagagagcaagtcctgttagccaactcttgatat	3721
Db	6439	TTGATTGACTTAAACCCATTCTGCTGACAGCCAGTCTGCTGACGCCAAATCTGTGATAT	6380
OY	3722	tcacaaagatgcaaccttgcacatctaga laaaagctctcagaagaagtaactgaga	3781
Db	6379	TCACAAAGAGATGCMACTTTGCATTCAGATAGATAAAAAAGTCTCAGSAAGTACTGAGAA	6320
OY	3782	tcacagaatatgattatctcgtatcttgaaggaaagaaagttcttgagagagcgactccat	3841
Db	6319	TCACAGAAATTAATTATATCCGATCTGTAAAGGAAGAAAGTCTTAGAGAGCGCAGTCCAT	6260
OY	3842	agaagaagtcacagagacctgcgaacaacccaattatctcacacacgaagccactatga	3901
Db	6259	AGAAAGGTACATGAGACCTCGGAAACACCCAAATTATTCACACAGCAGCAGCCCTATTGGA	6200
OY	3902	aaagtgtaacagtaacacatttttgaactcccttctacataagactccagaatgaagc	3961
Db	6199	AAAGTGACGATACCCACTTTTGTGACACTCTCCCTTTGATATATACATTCGCAGAGTGAAC	6140

Db 3979 AACGAGGTAATGAGCAATATTTGATGAGATATCCCTTTTGTGTGTGTG 3920
Qy 6182 Tgcatlaagttgtaacggtacatgaataaacaatgaagttctgtcctaataatgtagtg 6241
Db 3919 TGCATTAAGGTTGTAAGGTAACATGAAACAAATGAAGTTCTTGCTATATAGTAGG 3860
Qy 6242 aaaaagaagaagaatgaanaalattltagcclacttaggaanaaaggtagactia 6301
Db 3859 AAAACAAGAAGAAATGAATATTTTATGCTACTTAGGAAAAAAGGATGACACTTA 3800
Qy 6302 ttatctccgaagttcttt 6361
Db 3799 TTCAATTCAGAGTACTTTTATTTTATTTTATTTTAACTTAACTCAATGTTTAACTT 3740
Qy 6362 aagatataaataataatccctcttttttttttttttttttttttttttttttttttttt 6421
Db 3739 AAGATATTAACATATATATCCCTTTTATTTGCTTTGTCTATGTTCAATGAAACATTTG 3680
Qy 6422 agaaattattgataagtggtgtaacatgcaagcgtgat- tttttttgcatctg 6480
Db 3679 AGAAATTTATTTGATTAAGTGTTCCTGGAATCTGCAACGCTGATGTTTTTTCATTTG 3620
Qy 6481 taatgcatctgactcatttttaacttaattggaagttgctttgtatcattgtttgt 6540
Db 3619 TAGTGCATTTGCACCTCAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 3560
Qy 6541 ttgggtttgttt 6600
Db 3559 TTGGGTTTGTGTTTCTTTTCAAGTGGCGGCTGCTTTCTTAAATTTGATGCGAGGT 3500
Qy 6601 aaggttcaacagttcgtgactgttgtaggaatgaatgaanaaagtcttcttgatg 6660
Db 3499 AGAGTTCAACAGTTCGAGTGTGAGAGCAATGATPAAAAAATGCTTTTCGATG 3440
Qy 6661 ttgtgttgcatt 6720
Db 3439 TTGTGTGATTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCAT 3380
Qy 6721 aaagaagaagaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6780
Db 3379 AAGCAAGAGAGCAAGAAATGAGAGTAACTGCTGCTTCACTTTCATTTTAAAGCGGCT 3320
Qy 6781 talttgcattcactgtgtgtagtcttaataatcacaataactgaataaagaatgag 6840
Db 3319 TATTTGATCTCACCCTGACGCTGAGCTGATTAATTAATTAATTAATTAATTAATTAAT 3260
Qy 6841 aatgagagctttgacatcaaatatgtgtagtaatttcttcttcttcttcttcttcttct 6900
Db 3259 AATGAGAGGCTTTGACATTAATTTATGATGATTAATTTATCTTCTTGAATTTTGTAT 3200
Qy 6901 ggaatcatcacaatgtatagcagacttgagagtgacatgaatgaatgaatgaatga 6960
Db 3199 CGATGCATCTCAAAATGTATAGCCAGACTTGAGAGGTGACAAATTAAGATCAAAAGA 3140
Qy 6961 gaggagattcccccaacaatatttatttctttaglaaagaataaagaatga 7020
Db 3139 GAGGAGATTTCCCAACAAATATTTTATTTTCTTAAATTAAGATCAAAAGA 3080
Qy 7021 tctgtgcaatccttaagaacatatactatgtgtagcgtcttaataatgaacacaga 7080
Db 3079 TCGTGGCAATCTTAAACCAATATTAATGATGAGCTGCTTAAATGAGCAAAACCGAGA 3020
Qy 7081 agtttgttaacttggaacatatactgaatgaatgaatgaatgaatgaatgaatgaatga 7140
Db 3019 AGTTTGTGTTAACTTTGGCAATATGAGCAATATTAATTTTTCGCAAAACTACTCTTAA 2960
Qy 7141 caatttctctagtgtagcgaacaaatagttcttatttttttttttttttttttttttttt 7200
Db 2959 CAATTTCTATGTTGTGAGACCAAAATAGTTCTTAAATTTTTCGATGATGCTTTT 2900
Qy 7201 atttctatcaatt 7260
Db 2899 ATTTCATTCATTTTATTTTATTTTCTCAGACAGCAATGATGATGATGATGATGATGATG 2840

Qy 7261 aatacatatcactcttggaaatattatgtagcgtacttttgaataatattt 7320
Db 2839 AATCATATATCATATTTCTGAAATATTTATGAGTCACTTTTATGAGCAATATTTT 2780
Qy 7321 ggaatgcttgacagatagatcttattcattccttcttattatattgaatatttattt 7380
Db 2779 GGAATGCTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2720
Qy 7381 catlttcttcttcatatatacatatttggtaggaagagtttggcttttttga 7440
Db 2719 CATTTTGTCTTCAATATATATATTTTGGTGGAGAGAGGTTGGGCTTTTGTAAA 2660
Qy 7441 gagcaaaaattatataacacataacactccttttttggacataatlaagccttattc 7500
Db 2659 GAGCAAAAATTTATTTATTAACCTTAACACTCTTTTGAATTTGATTTTGAATTTTGA 2600
Qy 7501 catctcgaagatataataaataatttttttttttttttttttttttttttttttttttttt 7560
Db 2599 CATCTTCAGATATATTTTAAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAA 2540
Qy 7561 tcttaattgtgattttaaagagatatttggtaggaacttttttaatgaaggaatt 7620
Db 2539 TCTTAAATGTATTTTAAAGAGCTATATGATGAGAACTTTTAAATGAGAAATTT 2480
Qy 7621 catgtagatttaggaatttctccttggaagaagcttcccttgtagtgaataatgtag 7680
Db 2479 CATATATTTTAAATTTTCTTCTTGAAGAGCTTCCCTTGAGTAAATGATGATG 2420
Qy 7681 ccaagctaaatgtgtgcatattttaaagaacataatatttatttggctatatt 7740
Db 2419 CCAGCTTAAATTTGTGCAATTTTAAATGAAATTTTAAATTTTAAATTTTAAATTTTAA 2360
Qy 7741 ctaatttgagctttgatacactttagccagagacagctatgcttctcattcttctc 7800
Db 2359 CTAAATTTGAGCTTTGATCAAACTTTAGGCAAGAGAGAGCTATGCTTCTCTCTC 2300
Qy 7801 ttttctcacttcttctcctcactcactcctcgtatctatcttcttcttcttcttcttctt 7860
Db 2299 TTTTCTCAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2240
Qy 7861 aatcataaagaagccacacatctcagaagtttggattggaaggaacacatgac 7920
Db 2259 AATCATATAGAGCAACCATCTGAGAGCTTTGATGAGAGAGAGCTATGAGCTATGAGCT 2180
Qy 7921 caagatataagaagaagcagagctctaaatgtatcactgttagtcttaagaagaaga 7980
Db 2179 CAAGTATAG 2120
Qy 7981 gtagcccaattctctcactgacatgacatgagatttttttaacacttlaagatag 8040
Db 2119 GTATGCCCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2060
Qy 8041 tgaatgtcgttcttctcactgcttcttcttcttcttcttcttcttcttcttcttcttct 8100
Db 2059 TGAATGTCTGTTCTTAACTGTTCTGTTTGTGAGAGTGAATTTTAAATTAAGAGAG 2000
Qy 8101 gggatcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 8160
Db 1999 GGGATCTCTTCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1940
Qy 8161 gttgaagcctgtgtgtagcaattatgttlaaattgacatgtagacataatcattatg 8220
Db 1939 GTTGAAGCCTGTGAGAGCAATATGATTTATTTGACATGTCACATATCTATTTATG 1880
Qy 8221 atccaatgcaaatgaagctcccaaaaatattatgaatgaatgaatgaatgaatgaatgaatga 8280
Db 1879 ATCCAAATGAAATAGAGCTCCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1820
Qy 8281 aatatcatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 8340
Db 1819 AATATCATTTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1760

Dd	680	TGCCAATATTATTTATGTCGGCCAAAGGGCGCTTATTTAAACCTGCAGTTCCCAAGGCGACG	621
Qy	9473	aaaggttggggaactttctttaagaacagactgttaaalcaactaaggacaacatagt	9532
Dd	620	AAAGCTTGGGGTTCATTTTTCTTAAGAAGCGCCTGAATATCAACTTAGGACCATAGCT	561
Qy	9533	gttaccattgaagatgcgaacaacctatacttaagcgtgtanaatoagttctctaagtct	9592
Dd	560	GTTACTATGAAGATGCAAAACATTACTAGGCTGATATAATCATAGTTTCTTAATGGCT	501
Qy	9593	accaataagaacatatatocaaataaaoagccaattccctcttgaggcgacatttgca	9652
Dd	500	ACCATTATAGGCAAATATACAAITAAIPAACGCCAAATTCCTTGAGGGCGCATTTWTACA	441
Qy	9653	accaaatggaaaaactttgggggaagcatlaggggggaacatlocuaaalygcaatgttaa	9712
Dd	440	ACCAACATGGAATACTTTGGGGAGAGCGTATGAGGGGGGAACTCTCAAAATGCCAATGTAAA	381
Qy	9713	atttaacttaacgcgaatatccocagcagaaaaigtcttcotaatygaatgatattcagt	9772
Dd	380	ATTTAACCTTACGAAATATTCACACACAAANAATGTCTTCATATATGATGATTCANGT	321
Qy	9773	tgcctaaagaaagaatitaaatttgttagtcctgatttgaaataacgaatgttgccataat	9832
Dd	320	TGCTAAGAAAAAGATTCATTTGTATGTCCTGATTTGAAATCTAATGAAATTTGGCTAATAT	261
Qy	9833	agttctgtctctaacacacatgaaatlltcttgattacttaattcttgittctatagtc	9892
Dd	260	AGTTCTGTCTTACACACATGAAATTTTTCGTTTATTTATTTTGTTCATATAGTC	201
Qy	9893	attttatttctactccacaacactgtctctgtgtatltcttaaygaacaacatltoag	9952
Dd	200	ATTGTATTTCTACTCACAAACATGCTTCGTGATTTCTTATGCAAAACATCTTCAG	141
Qy	9953	cacgaagaagtgcctgttacactcraaaccttgataataagtttiaccccagttacacat	10012
Dd	140	CACCAAAAGATGCTTACTTACCTTAACCTTGAAATATAAGTTTATACACCGATTCACAT	81
Qy	10013	aacgcgctgtgatalggtlataagatlaacttccalcctclacgaacatlggaataac	10072
Dd	80	AACGCGCTGTGAAGCTTATATGATTCACCTTCATCCCTTCAG--CAATAGCAATATAC	23
Qy	10073	agatcatgttaatatatatata 10094	
Dd	22	AGATCATGTGTAATATATATATA 1	
 RESULT 13 PCT-US01-01334-6815/C Sequence 6815, Application PC/TUS0101334 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc., et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCT/JPCT CURRENT APPLICATION NUMBER: PCT/US01/01334 CURRENT FILING DATE: 2001-01-17 PRIOR APPLICATION NUMBER: 60/179,065 PRIOR FILING DATE: 2000-01-31 PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: 60/214,886 PRIOR FILING DATE: 2000-06-28 PRIOR APPLICATION NUMBER: 60/217,487 PRIOR FILING DATE: 2000-07-11 PRIOR APPLICATION NUMBER: 60/225,758 PRIOR FILING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/220,963 PRIOR FILING DATE: 2000-07-26 PRIOR APPLICATION NUMBER: 60/217,496 PRIOR FILING DATE: 2000-07-11 PRIOR APPLICATION NUMBER: 60/225,447 PRIOR FILING DATE: 2000-08-14			

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PRIOR APPLICATION NUMBER: 60/232,398

Query Match 56.2%; Score 5793; DB 1; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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5765 AACAAAGAAAGGCGCTTAAACCAGAGGCACTTCAAGCTGAGACAGCTAACAACAGCAGAG 5706
3542 gggcgaatagagagcaagtcaatggaagccggttagagagaggttcagaatcatct 3601
5705 GGGCGAATAGAGAGCAAGTCAATGAAGAGCCGCTTAGAGAGAGTCAAGAACATCAATCT 5646
3602 aactgaagtcaccagagagaaattccactcccaagcctlaagtaaatccgaagcccaagg 3661
5645 AACTGAAGTCACCAGAGAGAAATTCCACTCCAGCCTTAAGTAATACGAAGCCCAAGCG 5586
3662 ttcatgtactaaagccattctgtcagcagcagctcgtgtcagccaaactcggatct 3721
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3722 tcacaaagaatgcaacctttgacatctcgaatataaagaatccctcagaagttactggaga 3781
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5345 AAAGTACCAGTACCCACTTTTGTGACTCCCTTTGTACATATAGACTTCCAGAGGTGAAGC 5286
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4082 tctgctctctcatcttttaagctgttgatgaacaaatgacatctccttaagatttggcat 4141
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PRIOR APPLICATION NUMBER: 60/233,065
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PRIOR APPLICATION NUMBER: 60/232,398

Query Match 56.2% Score 5793; DB 30; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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QY 3482 aacaagaagcgttaacccaagcagcacttcagctgagcagcacaacaagcagag 3541
DB 5765 AACAGAAACCGCTTAAACCCAGAGCCTTCAAGCTGAGCAGCTCAACAAACAGAGAG 5706
QY 3542 gggcagcaatgagcagcaatgcaatggaagcccgtaagagagaggtcagaagatcat 3601
DB 5705 GGGCAGCAGTGAAGAGAGCAATTCACATCCCGACCTTAAGTAAATPACAGACCCAGAG 5646
QY 3602 aactgaagaatcaccaagagaatltccactccccaagccttaagtaataagaagccagag 3661
DB 5645 AACTGAAGATCACAGAGAGAAATTCACATCCCGACCTTAAGTAAATPACAGACCCAGAG 5586
QY 3662 ttatgtactaaagcacttcgtcagcagcagcagtcctgggtcagccaactctggat 3721
DB 5585 TTGATGTACTAAAGCCATTCGTCTGAGCAGCAGCTGCTGATCAGCCAACTCTGATAT 5526
QY 3722 tcacaaagatgcaaccttgacacttaagataaagaagtcctcagaagaagtactggaga 3781

DB 5525 TCACAAAAGATGCAACCTTTGCACATTCAGATTAAGAAAAATCTCTCAGAAAGTACTGAGA 5466
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Db 2585 TTGCTGTGCTATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTT 2526
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Q	8521	ttaaagttgagaggagtgcaactttagctactgctgttgttggtagaacatgagc-aaaa	8579
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RESULT 15
US-10-092-400-6815/c
; Sequence 6815, Application US/10092400
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010CI
; CURRENT APPLICATION NUMBER: US/10/092,400
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
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; PRIOR APPLICATION NUMBER: 60/220,963
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PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065

Query Match 56.2% Score 5793; DB 37; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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QY 3482 aacagaagaagccttaaccagagagcattcagctgagcagctcaacaaacagcagag 3541

DB 5765 AACAGAAAGCCCTTTAAACAGAGGCACTTCAAGCTGAGCTCAACAAACAGAGAG 5706
QY 3542 gggcagcaatgagagcaagcaatggaagccgttaaggagggggtccagaatattc 3601
DB 5705 GGGCAGCAATGAGAGGCAAGTCAATGGAAGCCGTTTAGAGAGAGGTCACAAATCATCT 5646
QY 3602 aactgaagtcacagaagaatctccatcccgccgaagtaataaagccagag 3661
DB 5645 AACTGAAGTCAACAGAGAGAAATTCACCTCCAGCCCAAGTAAATACGAAGCCAGGG 5586
QY 3662 ttattgactaaagcaattctctcgaagccagtcctgagcccaacttgatata 3721
DB 5585 TTATTGACTTAAAGCACTTCTGTCAGAGCAGCTGCTGAGCCAACTTGATAT 5526
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RESULT 3
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: Sequence 1452, Application US/10172118
: GENERAL INFORMATION:
: APPLICANT: Dai, Hongyue
: APPLICANT: He, Yudong
: APPLICANT: Linsley, Peter
: APPLICANT: Mao, Mao
: APPLICANT: Roberts, Chris
: APPLICANT: Van 't Veer, Laura
: APPLICANT: Van de Vijver, Marc
: APPLICANT: Bernards, Rene
: TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
: FILE REFERENCE: 9301-175-999
: CURRENT APPLICATION NUMBER: US/10/172,118
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 60/380,770
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 2699
: SEQ ID NO 1452
: LENGTH: 10011
: TYPE: DNA
: ORGANISM: Homo sapiens
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: NM_014112
: DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1452

Query Match 97.1%, Score 10011; DB 6; Length 10011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-10-022-486-58
Sequence 58, Application US/10022486
GENERAL INFORMATION:
APPLICANT: Hall, Jonathan
APPLICANT: Kinzel, Bernd
APPLICANT: Nall, Francois
APPLICANT: Meller, Jan
TITLE OF INVENTION: Antisense Oligonucleotides Directed to
TITLE OF INVENTION: Itapoxin A Regulated Genes
FILE REFERENCE: 4-31674A
CURRENT APPLICATION NUMBER: US/10/022,486
CURRENT FILING DATE: 2001-12-13
PRIOR APPLICATION NUMBER: 60/255,591
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 179
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 1914
TYPE: DNA
ORGANISM: Homo sapiens
US-10-022-486-58

Query Match 18.1%; Score 1864.4; DB 6; Length 1914;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY 5008 cttctctcatggtcattgttcagaatttgaacctagaatgcgagctgtgttaaggcttg 5067
Db 194 cttctctcatggtcattgttcagaatttgaacctagaatgcgagctgtgttaaggcttg 253
QY 5068 gttagaattgcaagcaacatgacagatgtgtgcacgctgtttttaccacgctgcct 5127
Db 254 gttagaattgcaagcaacatgacagatgtgtgcacgctgtttttaccacgctgcct 313
QY 5128 gtacatacacatgacacccctctgtatatttgcctttagatgttcaactacacag 5187
Db 314 gtacatacacatgacacccctctgtatatttgcctttagatgttcaactacacag 373
QY 5188 agtctcttggcttgggtttatgattcattgttgcacacatgtacacatttaaaaaa 5247
Db 374 agtctcttggcttgggtttatgattcattgttgcacacatgtacacatttaaaaaa 433
QY 5248 atgtctcgaatgcttctgtagatgttcatattttagcaggaatttcttcttctgtgta 5307
Db 434 atgtctcgaatgcttctgtagatgttcatattttagcaggaatttcttcttctgtgta 493
QY 5308 tgaacagatgagatttgccttcttaagctcctgttggtaactaactacactgtgaca 5367
Db 494 tgaacagatgagatttgccttcttaagctcctgttggtaactaactacactgtgaca 553
QY 5368 ttataactaaggaatccctcaatctcaataaagcatagatgatacaatgtcagacctg 5427

Db 554 ttataactaaggaatccctcaatctcaataaagcatagatgatacaatgtcagacctg 613
QY 5428 ggtttaatttggtagacacatgacatttcttcaaggtaaccgctgtatttalla 5487
Db 614 ggtttaatttggtagacacatgacatttcttcaaggtaaccgctgtatttalla 673
QY 5488 tttcttggtagaataataatttccaaacttgggttcagcagcgtcttaaggcttaagt 5547
Db 674 tttcttggtagaataataatttccaaacttgggttcagcagcgtcttaaggcttaagt 733
QY 5548 taccacagactggaagttgtgtata-gtaccagccaatcccttaacttaagtatacagat 5607
Db 734 taccacagactggaagttgtgtata-gtaccagccaatcccttaacttaagtatacagat 793
QY 5608 ttagttaagtagcatlaaataagatttcttagaagatgcttccatlaagacttttaact 5667
Db 794 ttagttaagtagcatlaaataagatttcttagaagatgcttccatlaagacttttaact 853
QY 5668 taaggcttggtaaaaaactatcatgaagggaagcctctcagataactgctcaaggaa 5727
Db 854 taaggcttggtaaaaaactatcatgaagggaagcctctcagataactgctcaaggaa 913
QY 5728 taggcttaataaactgaacatttaataatgtgttaaggtgtgtagtgcagcctcaat 5787
Db 914 taggcttaataaactgaacatttaataatgtgttaaggtgtgtagtgcagcctcaat 973
QY 5788 gcttgctacaagagatgcatgacagcagcacttaatttgattgattatgttccca 5847
Db 974 gcttgctacaagagatgcatgacagcagcacttaatttgattgattatgttccca 1033
QY 5848 accagtagtttaatttctgcacagcagatgaagaatatactaaagctactgtagaac 5907
Db 1034 accagtagtttaatttctgcacagcagatgaagaatatactaaagctactgtagaac 1093
QY 5908 gtacagtaactatttcttaataaagctgtgggaacaaataggaataaataaacttat 5967
Db 1094 gtacagtaactatttcttaataaagctgtgggaacaaataggaataaataaacttat 1153
QY 5968 ttctctaglaaataataatgcatlcatlcaataatgtgtcctgacataatlaaata 6027
Db 1154 ttctctaglaaataataatgcatlcatlcaataatgtgtcctgacataatlaaata 1213
QY 6028 tattt.ctacagtgtaagatgacacaaagatattccatcatgacattagaatcagcttg 6087
Db 1214 tattt.ctacagtgtaagatgacacaaagatattccatcatgacattagaatcagcttg 1273
QY 6088 gctctgctagctgtttatatttgaatttgaatgtgacaaacaggtatgaagcaactatcc 6147
Db 1274 gctctgctagctgtttatatttgaatttgaatgtgacaaacaggtatgaagcaactatcc 1333
QY 6148 tatgcaagtagatacttcttgggtgtgtgtgtgcatgaagtgtgaacaggtacat 6207
Db 1334 tatgcaagtagatacttcttgggtgtgtgtgtgcatgaagtgtgaacaggtacat 1393
QY 6208 gaaacaaatgaagttcttgcataatgtgataatgtgaacaaagaaatgaataatt 6267
Db 1394 gaaacaaatgaagttcttgcataatgtgataatgtgaacaaagaaatgaataatt 1453
QY 6268 ttatgctacttaggaaaaaaagggttagcactatcatctcaagtactttttttttt 6327
Db 1454 ttatgctacttaggaaaaaaagggttagcactatcatctcaagtactttttttttt 1513
QY 6328 aatttthaagcttctaactacatgttataagctttagaagatgaacacataactctt 6387
Db 1514 aatttthaagcttctaactacatgttataagctttagaagatgaacacataactctt 1573
QY 6388 tatgtctgtctatagtttcatatgaacaattcaagaattatttgaatagttgtgctg 6447
Db 1574 tatgtctgtctatagtttcatatgaacaattcaagaattatttgaatagttgtgctg 1633
QY 6448 gaatctgcaagctgat-ttttttgcattctgtatgtcgaatttgcacccattttac 6506

Qy	8862	ctctcggaaatctctcggcggaagatgtgcaagatgtaacatgtaactgtgaagaatggtgaat	9021
Db	1	ctctcggaaatgctctcggcggaagatgtgcaagatgtaacatgtaactgtgaagaatggtgaat	60
Qy	9022	tcaagagtaatccacacgtggaagaaactagaacaatgacatctgtgttccttgaagaag	9081
Db	61	tcaagagtaatccacacgtggaagaaactagaacaatgacatctgtgttccttgaagaag	120
Qy	9082	aaagggagacgtgtaagcttaactctgttctccaaacgcggagaagaagaagaaacttllac	9141


```

Query Match: 4.4% Score 450.4; DB 7; Length 486;
Best Local Similarity 93.48; Pct. No. 2.9e-11;
Matches 454; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 4061 tggctctatccaccttcattgctgcctccatttcagctgttgatcagcaatga 4120
||||| |||||||

```

```

RESULT      8
US-09-918-995-22235
? Sequence 22235, Application US/09918995
? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc.
? TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
? TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
? FILE REFERENCE: 20411-756
? CURRENT APPLICATION NUMBER: US/09/918,995
? CURRENT FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: US/09/235,076
? PRIOR FILING DATE: 1999-01-20
? NUMBER OF SEQ ID NOS: 38054
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 22235
? LENGTH: 486
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(486)
? OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22235

```

Query Match	4.38	Score 444	DB 5	Length 486
Best Local Similarity	99.88	Pred. NO. 4.1e-70		
Matches 444	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 6771	taacggccattctcatctcaccctgcgcgtacgtcctataattccaataactggaat	6630		
Db 42	taacggccattctcatctcaccctgcgcgtacgtcctataattccaataactggaat	101		
QY 6831	aagaagcggagatagaagagcttgacatccaattatgtaattatattcctctag	6890		
Db 102	aagaagcggagatagaagagcttgacatccaattatgtaattatattcctctag	161		
QY 6891	gaatttgatgatcgtccccaattgtatgcgaacgttaaaccttacacattaaatgaat	650		

```

Db 162 gatttttgatgacgtcccaaaagtataagccagacttgagaggtgacaattaaagt 221
Qy 6951 ctaaaaagagagagatllcccccaaacacataattttcttaagaagaata 7010
Db 222 ctaaaaagagagagatllcccccaaacacataattttcttaagaagaata 281
Qy 7011 acagatgcatcgtggcaatccttaagcaacattactatgtgactgttaacga 7070
Db 282 acagaalgcacgtggcaatccttaagcaacattactatgtgactgttaacga 341
Qy 7071 aaacccagaagtttggttaacttgggaatataacagatattacttttgggcaaac 7130
Db 342 aaacccagaagtttggttaacttgggaatataacagatattacttttgggcaaac 401
Qy 7131 actcatalaagaatllctctagtgctgcgacacaataagttcttattttggcagt 7190
Db 402 actcatalaagaatllctctagtgctgcgacacaataagttcttattttggcagt 461
Qy 7191 atgcctttatttccatcaatt 7215
Db 462 atgcctttatttccatcaatt 486

```

RESULT 9

```

US-09-918-995-10414
; Sequence 10414, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10414
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10414

```

Query Match

```

Best Local Similarity 4.2%; Score 435.8; DB 5; Length 476;
Matches 440; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

```

Qy 4661 agagagataatggtcgaatgagaagatgagatggttaaacatcaacttttaaac 4720
Db 24 agagcancnccnagncnmgagaaatggaagatggaatacaacttttaaac 83
Qy 4721 tctaagtcataaacacatcttgctaatactgactgggaataatccataagaata 4780
Db 84 tctaagtcataaacacatcttgctaatactgactgggaataatccataagaata 143
Qy 4781 ccagactagaattatataattataagaagaagacccaactgtltagaattgaag 4840
Db 144 ccagactagaattatataattataagaagaagacccaactgtltagaattgaag 203
Qy 4841 gttacatatataactaagaagcagatgactgagccatctggacattgttcca 4900
Db 204 gttacatatataactaagaagcagatgactgagccatctggacattgttcca 263
Qy 4901 cccataaattgttgccataaattataaalgatcatgaacccttaggcagagagga 4960
Db 264 cccataaattgttgccataaattataaalgatcatgaacccttaggcagagagga 323

```

```

Qy 4961 tgaagtcagggcagatgaagaataatggcgccctccattagtcttctcattgg 5020
Db 324 tgaagtcagggcagatgaagaataatggcgccctccattagtcttctcattgg 383
Qy 5021 ccatgttccagatttgaactagaatgcagctgtgttgtaggttgtaggaagcg 5080
Db 384 ccatgttccagatttgaactagaatgcagctgtgttgtaggttgtaggaagcg 443
Qy 5081 aagcaacatgacagatggttgacagctgtttt 5113
Db 444 aagcaacatgacagatggttgacagctgtttt 476

```

RESULT 10

```

US-09-918-995-19024/c
; Sequence 19024, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19024
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-19024

```

Query Match

```

Best Local Similarity 3.6%; Score 374.8; DB 5; Length 379;
Matches 376; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 8751 gcaaatgagaagaagatagaagacgcccgcgacttggagggcattgtatttc 8810
Db 378 gcaaatgagaagaagatagaagacgcccgcgacttggagggcattgtatttc 319
Qy 8811 caaagaagaagcggcgaagcagagcattcttgcagagacattccttggatt 8870
Db 318 caaagaagaagcggcgaagcagagcattcttgcagagacattccttggatt 259
Qy 8871 ttcagtaacttccatagacagatggctcacatgtcttcgatagtgctgcagttg 8930
Db 258 ttcagtaacttccatagacagatggctcacatgtcttcgatagtgctgcagttg 199
Qy 8931 aaagcatcccaattaatgtcagtaattagaactcttgaatatgtcaggaagatg 8990
Db 198 aaagcatcccaattaatgtcagtaattagaactcttgaatatgtcaggaagatg 139
Qy 8991 tcaagtatgccaatgaagaataatgtgaattcaagaagatccacacgtgagaactag 9050
Db 138 tcaagtatgccaatgaagaataatgtgaattcaagaagatccacacgtgagaactag 79
Qy 9051 acaatgtacatcatatgttctcttgaagaagaagagagctgttaactcactcgtc 9110
Db 78 acaatgtacatcatatgttctcttgaagaagaagagagctgttaactcactcgtc 19
Qy 9111 ctacacggagaaaagca 9128
Db 18 ctacacggagaaaagca 1

```

RESULT 11

```

US-09-539-800C-18053
; Sequence 18053, Application US/09539800C
; GENERAL INFORMATION:
; APPLICANT: Seligman, Jeffrey J.
; APPLICANT: Deleane, Angelo M.

```

```
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/943,979
PRIOR FILING DATE: October 4, 1997
PRIOR APPLICATION NUMBER: 60/027,782
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 18053
LENGTH: 314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incycle ID No: hu01112257
US-09-539-800C-18053
```

```
Query Match 2.9%; Score 296.4; DB 5; Length 314;
Best Local Similarity 98.0%; Pred. No. 9.2e-44;
Matches 300; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6465 ttttttgcattcgtgtagtcgacattgcacatcatttaacatlaattcgcagttgctt 6524
DB 9 ttttttgcattcgtgtagtcgacattgcacatcatttaacatlaattcgcagttgctt 68
QY 6525 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttttt 6584
DB 69 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttttt 128
QY 6585 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgtgtgtgtgtgtgtgtgtgtgt 6644
DB 129 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgtgtgtgtgtgtgtgtgtgtgt 188
QY 6645 aaatgtcttcgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6704
DB 189 aaatgtcttcgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 248
QY 6705 aaaaaagagaaagagaaagagagagagagagagagagagagagagagagagagagagag 6764
DB 249 aaaaaagagaaagagagagagagagagagagagagagagagagagagagagagagagag 6764
QY 6765 catgtt 6770
DB 309 catgtt 314
```

```
RESULT 12
US-09-539-800C-17062
Sequence 17062, Application US/09539800C
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 17062
LENGTH: 302
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incycle ID No: hu01255098
US-09-539-800C-17062
```

```
Query Match 2.9%; Score 294; DB 5; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.5e-43;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6465 ttttttgcattcgtgtagtcgacattgcacatcattttacatlaattcgcagttgctt 6524
DB 9 ttttttgcattcgtgtagtcgacattgcacatcattttacatlaattcgcagttgctt 68
QY 6525 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttttt 6584
DB 69 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttttt 128
QY 6585 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgtgtgtgtgtgtgtgtgtgtgt 6644
DB 129 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgtgtgtgtgtgtgtgtgtgtgt 188
QY 6645 aaatgtcttcgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6704
DB 189 aaatgtcttcgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 248
```

QY 6705 aaaaagagaaagagaaagacagaacaaatcagagactaaagtcgctt 6758
|||||
Db 249 aaaaagagaaagagaaagacagaacaaatcagagactaaagtcgctt 302

RESULT 13

US-09-539-800C-17109
Sequence 17109, Application US/09539800C
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Sluve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 17109
LENGTH: 293
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01300652
US-09-539-800C-17109

Query Match 2.8%; Score 285; DB 5; Length 293;
Best Local Similarity 100.0%; Pred. No. 9,9e-42;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6465 ttttttgcattctgtagtcgaattgcactcatttcaattcaatttcgagttgctt 6524
|||||
Db 9 ttttttgcattctgtagtcgaattgcactcatttcaattcaatttcgagttgctt 68
QY 6525 tgcatactgtttgtttgtttgtttgttttttcaagagtcgagttcttctta 6584
|||||
Db 69 tgcatactgtttgtttgtttgtttgttttttcaagagtcgagttcttctta 128
QY 6585 aagttgagtagcaggtagagttcaacacagttctgagcttctgtagcagaagaattaaaa 6644
|||||
Db 129 aagttgagtagcaggtagagttcaacacagttctgagcttctgtagcagaagaattaaaa 188

QY 6645 aaatgtcttcgagatgtgtgttgcatttcaatttgcattttttgtttgatatata 6704
|||||
Db 189 aagttcttcgagatgtgtgttgcatttcaatttgcattttttgtttgatatata 248

QY 6705 aaaaagagaaagagaaagacagaacagaacaaatcagagactaaat 6749
|||||
Db 249 aaaaagagaaagagaaagacagaacagaacaaatcagagactaaat 293

RESULT 14

US-09-539-800C-14916
Sequence 14916, Application US/09539800C
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Sluve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 14916
LENGTH: 269
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01062430
US-09-539-800C-14916

Query Match 2.5%; Score 261; DB 5; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-539-8068-2497
Sequence 2497, Application US/095398068
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura J.
APPLICANT: Mullaby, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
FILE REFERENCE: PD-1027 CIP
CURRENT APPLICATION NUMBER: US/09539, 8068
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/706, 766
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/004, 676
PRIOR FILING DATE: October 2, 1995
PRIOR APPLICATION NUMBER: 08/749, 515
PRIOR FILING DATE: November 15, 1996
PRIOR APPLICATION NUMBER: 60/006, 810
PRIOR FILING DATE: November 15, 1995
PRIOR APPLICATION NUMBER: 08/822, 285
PRIOR FILING DATE: March 20, 1997
PRIOR APPLICATION NUMBER: 60/013, 696
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PRIOR APPLICATION NUMBER: 08/951, 197
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PRIOR APPLICATION NUMBER: 08/826, 438
PRIOR FILING DATE: March 20, 1997
PRIOR APPLICATION NUMBER: 60/016, 145
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PRIOR APPLICATION NUMBER: 08/993, 402
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SEQ ID NO 2497
LENGTH: 253
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ORGANISM: Homo sapiens
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NAME/KEY: misc-feature
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NAME/KEY: unsure
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OTHER INFORMATION: a, t, c, g, or other
US-09-539-8068-2497

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Search completed: July 22, 2002, 01:15:30
 Job time: 25977 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: July 21, 2002, 14:58:48 ; Search time 12014.9 Seconds
(without alignments)
17965.795 Million cell updates/sec

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10315
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Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb.htg:*
3: gb.in:*
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33: em.htgo.in:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6595.6	63.9	159305	2	AC013815	Homo sapi
4	5295	51.3	5507	9	AF264784	Homo sapi
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6	2486.4	24.1	2596	5	AK009948	Mus muscu
7	2295	22.2	4625	5	AF346838	Homo sapi
8	1580.6	15.3	1587	9	AK021511	Homo sapi
9	1537	14.9	1551	9	AK021470	Homo sapi
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11	1306	12.7	3767	5	AF346837	Homo sapi
12	1139.4	11.0	82724	2	AC084171	Homo sapi
13	1139.4	11.0	310002	9	AF178030	Homo sapi
14	1116	10.8	165191	2	AC103571	Homo sapi
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16	771.2	7.5	113725	2	AC106815	Sequence
17	761.4	7.4	766	6	AX113088	Rattus no
18	668.8	6.5	674	6	AX067327	Sequence
19	460.8	4.5	350000	9	AF130342	Sequence
20	457.6	4.4	113725	2	AC106815	Sequence
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22	258.4	2.5	67407	2	AC013789	Sequence
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33	77.8	0.8	12405	6	AX251840	Sequence
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37	77.4	0.8	5126	6	AX348926	Sequence
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45	76.2	0.7	99003	2	AL390756	Homo sapi

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VERSION	AF183810.1				
KEYWORDS					
SOURCE					
ORGANISM					

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 10011)

REFERENCE

1 (bases 1 to 10011)

AUTHORS

Momeni, P., Glockner, G., Schmidt, O., von Holtum, D., Albrecht, B.,

TITLE

Gillesen-Kaesbach, G., Hennekam, R., Meinecke, P., Zabel, B.,

JOURNAL

Mutations in a new gene, encoding a zinc-finger protein, cause

MEDLINE

Tricho-rhino-phalangal syndrome type I

AUTHORS

2 (bases 1 to 10011)
Momeni, P., Glockner, G., Schmidt, O., von Holtum, D., Albrecht, B.,

Gillesen-Kaesbach, G., Hennekam, R., Meinecke, P., Zabel, B.,

TITLE
Direct Submission
Submitted (06-SEP-1999) Institut fuer Humangenetik,
JOURNAL
Universitaetsklinikum, Hufelandstr. 55, D-45121 Essen, Germany
FEATURES
Location/Qualifiers
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BASH COUNT 3067 a 1963 c 2056 g 2925 t
ORIGIN

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PROGRESS ***, 4 ordered pieces.
ACCESSION AC013815
VERSION AC013815.11 GI:18252021
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULFILL; HTGS_ACTIVEIN.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 165813)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

MON

~~UOW~~

	Db	63802	ATTTCAGCTACGACAAATTTATCCACGACGAAAATGGTCTTCAATATGGAATGATTCANGT	63743
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DEFINITION	Homo sapiens zinc finger protein GC79 mRNA, complete cds.			Pri 05-OCT-2000
ACCESSION	AF264784			
VERSION	AF264784.1	GI:10644121		
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SOURCE	human.			
ORGANISM	Homo sapiens			
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 5507)			
AUTHORS	Chang,G.T.G., Steenbeek,M., Schippers,E., Blok,L.J., van Weerden,W.M., van Alewijk,D.C., Eussen,B.H., van Steenbrugge,G.J. and Brinkmann,A.O.			
TITLE	Characterization of a Zinc-Finger Protein and Its Association With Apoptosis In Prostate Cancer Cells			
JOURNAL	J. Natl. Cancer Inst. 92 (17), 1414-1421 (2000)			
PUBMED	10974077			
REFERENCE	2 (bases 1 to 5507)			
AUTHORS	Chang,G.T.G.			
JOURNAL	Direct Submission			
	Submitted (09-MAY-2000) Endocrinology & Reproduction, Erasmus University Rotterdam, P.O.Box 1738, Rotterdam 3000 DR, Netherlands			
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: July 21, 2002, 15:59:38 ; Search time 948.56 Seconds
(without alignments)

16670.377 Million cell updates/sec

Title: us-09-702-216-1

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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
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	2	10255	99.4	10319	21	AACT74759	Breast cancer protein
	3	9951	96.5	10006	22	AAAD0861	Human ORFX ORF14
C	4	6774.6	65.7	10246	22	ABAI1485	Human breast cancer
C	5	6587.2	63.9	10004	22	ABAI1483	Human nervous syst
C	6	5793	56.2	5825	22	ABAI1484	Human nervous syst
7	2486.4	24.1	2596	22	AAH13738	Human CDNA sequenc	
8	2257.6	21.9	2327	22	AAAD06845	Human breast cancer	
9	1580.6	15.3	1587	22	AAH16992	Human CDNA sequenc	

10	1537	14.9	1551	22	AAH15234	Human cDNA sequenc
11	1007	9.8	1009	21	AACT79479	cDNA sequence for
12	943.4	9.1	996	22	AACT4852	Human breast cancer
13	761.4	7.4	766	22	AAH82511	Human breast tumor
14	681.6	6.6	691	22	AAH03367	Human cDNA clone (
15	668.8	6.5	674	22	AAH44875	Human breast cancer
16	648.6	6.3	813	22	AAH03487	Human cDNA clone (
17	630	6.1	649	22	AAH03278	Human cDNA clone (
18	621	6.0	664	22	AAH11067	Human nervous syst
19	577.2	5.6	633	22	AAH21431	Human breast cancer
20	541.6	5.3	569	22	AAH08818	Human cDNA clone (
21	527.4	5.1	582	22	AAH12558	Human breast cancer
22	520.8	5.0	560	22	AAH08905	Human cDNA clone (
23	474.6	4.6	572	22	AAH09024	Human cDNA clone (
24	453.4	4.4	460	22	AAH21573	Human breast cancer
25	428.4	4.2	451	22	AAH12700	Human breast cancer
26	402	3.9	438	22	AAH20878	Human breast cancer
27	388	3.8	430	22	AAH11991	Human breast cancer
28	384.6	3.7	426	22	AAH23557	Human breast cancer
29	377.4	3.7	415	22	AAH25185	Human breast cancer
30	347.2	3.4	357	22	AAH17790	Human breast cancer
31	345	3.4	357	21	AAH16523	Human secreted pro
32	343	3.3	344	22	AAH10715	Human breast cancer
33	315.6	3.1	831	22	AAH16342	Human breast cancer
34	315.4	3.1	333	19	AAH27248	Human breast cancer
35	315.4	3.1	333	22	AAH45166	Human breast cancer
36	275.4	2.7	305	22	AAH55585	Human breast tumor
37	265.6	2.6	558	22	AAH24203	Human breast cancer
38	236.8	2.3	248	22	AAH09195	Human breast cancer
39	236.8	2.3	248	22	AAH09198	Human breast cancer
40	236.8	2.3	248	22	AAH17084	Human breast cancer
41	236.8	2.3	248	22	AAH17087	Human breast cancer
42	210	2.0	258	22	AAH16331	Human breast cancer
43	208	2.0	209	22	AAH25174	Human breast cancer
44	205	2.0	241	22	AAH14695	Human breast cancer
45	200.2	1.9	375	22	AAH19807	Human breast cancer

ALIGNMENTS

RESULT	1
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ID	XX
AC	AAAS4123;
DT	08-FEB-2001 (first entry)
DE	Breast cancer protein BCN2 coding sequence.
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KW	Breast cancer; diagnosis; prognosis; detection; screening;
KW	antibody; oestrogen receptor; anti-oestrogen; immune response;
KW	lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCL1; BCN1; BCN2;
KW	BCN5; BCQ2; BCN2; BCR3; BCR2; BCR7; BCY3; human; ds.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
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XX	
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PF	15-MAR-2000; 2000WO-US06952.
XX	
PR	15-MAR-1999; 99US-0268865.
PR	12-NOV-1999; 99US-0439878.
PR	12-NOV-1999; 99US-0440370.
PR	15-NOV-1999; 99US-0440493.

Query Match	Best Local Similarity	Score	DB	Length
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